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cgtaggcttga	gtacgcactg	ccagtaaggt	gtgtgatgtg	atg	gaa	ata	agt	gtc										115
				Met	Glu	Ile	Ser	Val										
				1				5										
ttg	atc	atc	gcc	gca	ctg	atc	ttg	gtg	gca	ggc	atc	gta	ctg	tgg	cgc		163	
Leu	Ile	Ile	Ala	Ala	Leu	Ile	Leu	Val	Ala	Gly	Ile	Val	Leu	Trp	Arg			
			10						15					20				
gcg	gac	tcg	tct	aaa	cag	gca	gct	aaa	aag	gct	gaa	tca	cct	gtg	ggc		211	
Ala	Asp	Ser	Ser	Lys	Gln	Ala	Ala	Lys	Lys	Ala	Glu	Ser	Pro	Val	Gly			
			25					30					35					
tca	gtc	gca	cct	gcg	ccc	gtg	ctg	gtt	gaa	gaa	gag	ccg	gac	cct	gag		259	
Ser	Val	Ala	Pro	Ala	Pro	Val	Leu	Val	Glu	Glu	Glu	Pro	Asp	Pro	Glu			
		40					45					50						
ttt	gag	cca	gaa	ctg	gac	cct	gaa	cca	gaa	gcg	caa	cca	gaa	cca	gag		307	
Phe	Glu	Pro	Glu	Leu	Asp	Pro	Glu	Pro	Glu	Ala	Gln	Pro	Glu	Pro	Glu			
	55					60					65							
ctg	gaa	gtt	gcg	cct	aga	ttt	gcg	cca	gaa	cca	gtt	caa	gat	ctt	gag		355	
Leu	Glu	Val	Ala	Pro	Arg	Phe	Ala	Pro	Glu	Pro	Val	Gln	Asp	Leu	Glu			
70					75					80				85				
ccg	gat	cag	gct	gag	gac	att	tat	ttt	gat	gat	tcc	cct	gaa	ctc	gat		403	
Pro	Asp	Gln	Ala	Glu	Asp	Ile	Tyr	Phe	Asp	Asp	Ser	Pro	Glu	Leu	Asp			
				90					95					100				
gct	gat	gtt	gaa	aat	gcc	ttg	gct	gag	ctt	act	gag	gta	gaa	gac	tac		451	
Ala	Asp	Val	Glu	Asn	Ala	Leu	Ala	Glu	Leu	Thr	Glu	Val	Glu	Asp	Tyr			
			105					110					115					
ccg	gaa	gag	cca	gtg	cag	tct	gag	caa	cct	caa	gcc	cct	gcc	acg	gcg		499	
Pro	Glu	Glu	Pro	Val	Gln	Ser	Glu	Gln	Pro	Gln	Ala	Pro	Ala	Thr	Ala			
		120					125				130							
gag	gta	gct	gcg	gac	gag	gag	caa	cgg	ggc	gtc	gat	aag	cat	tcg	ttt		547	
Glu	Val	Ala	Ala	Asp	Glu	Glu	Gln	Arg	Gly	Val	Asp	Lys	His	Ser	Phe			
135					140					145								
ttg	agc	tct	ttg	cct	ggt	tcg	cag	cgc	cgg	gag	cgc	cga	aac	tgg	gcg		595	
Leu	Ser	Ser	Leu	Pro	Gly	Ser	Gln	Arg	Arg	Glu	Arg	Arg	Asn	Trp	Ala			
150					155					160					165			
gcg	aag	cac	cac	ttc	gat	ttc	atc	aag	gaa	gat	gcc	ttt	ttg	acc	gat		643	
Ala	Lys	His	His	Phe	Asp	Phe	Ile	Lys	Glu	Asp	Ala	Phe	Leu	Thr	Asp			
				170					175					180				

gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg 691
 Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val
 185 190 195

gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg 739
 Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala
 200 205 210

ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc 787
 Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val
 215 220 225

att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa 835
 Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu
 230 235 240 245

tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc 883
 Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu
 250 255 260

agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg 931
 Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr
 265 270 275

tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa 978
 Ser Val Trp Ile Pro Cys Gln Lys Leu
 280 285

tct 981

<210> 530

<211> 286

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 530

Met Glu Ile Ser Val Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly
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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
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Glu Ser Pro Val Gly Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu
 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
 260 265 270

Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu
 275 280 285

<210> 531
 <211> 1545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1522)
 <223> RXC01693

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gtcccaacaa ttgccagaac ccgaacacta ggcttgaacc atg aat act gca cct 115
 Met Asn Thr Ala Pro
 1 5

ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
 Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
 10 15 20

ccc tgg caa ggt gag gaa gcc ccc aac cct gag ctc gtg att tta aat 211
 Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
 25 30 35

gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
 Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
 40 45 50

cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307

Pro	Glu	Gly	Val	Gln	Phe	Leu	Leu	Gly	Leu	Asn	Pro	Glu	Pro	Leu	Thr		
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aaa	gca	gtt	gcg	cag	gcc	tat	tcc	ggc	cac	caa	ttc	gga	cag	ttt	gtg	355	
Lys	Ala	Val	Ala	Gln	Ala	Tyr	Ser	Gly	His	Gln	Phe	Gly	Gln	Phe	Val		
70					75					80					85		
gca	agc	ctt	ggt	gat	ggc	cga	gcg	ctt	ctt	ctc	ggc	gaa	gcc	cgc	tca	403	
Ala	Ser	Leu	Gly	Asp	Gly	Arg	Ala	Leu	Leu	Leu	Gly	Glu	Ala	Arg	Ser		
				90				95						100			
gct	gac	ggc	gta	ctg	cat	gat	atc	cac	ctc	aaa	gga	tct	gga	cga	acc	451	
Ala	Asp	Gly	Val	Leu	His	Asp	Ile	His	Leu	Lys	Gly	Ser	Gly	Arg	Thr		
			105				110						115				
caa	ttc	tcc	cga	gga	gcc	gat	gga	cgc	gcc	gtc	ctt	ggc	ccc	gtc	tta	499	
Gln	Phe	Ser	Arg	Gly	Ala	Asp	Gly	Arg	Ala	Val	Leu	Gly	Pro	Val	Leu		
			120				125					130					
cgc	gaa	tac	atc	atc	tcc	gaa	gcg	atg	cat	gca	ctt	ggt	gtt	ccc	acc	547	
Arg	Glu	Tyr	Ile	Ile	Ser	Glu	Ala	Met	His	Ala	Leu	Gly	Val	Pro	Thr		
	135					140					145						
acc	agg	tca	ctt	gca	gta	att	agc	acc	ggt	agg	aaa	atc	caa	cga	gga	595	
Thr	Arg	Ser	Leu	Ala	Val	Ile	Ser	Thr	Gly	Arg	Lys	Ile	Gln	Arg	Gly		
150				155					160						165		
agc	gta	gcc	cca	ggc	gca	gtc	ctt	gtt	cga	gta	gca	acc	agc	ctc	att	643	
Ser	Val	Ala	Pro	Gly	Ala	Val	Leu	Val	Arg	Val	Ala	Thr	Ser	Leu	Ile		
			170						175					180			
cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggt	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
			200				205					210					
gta	gct	gaa	cta	tcc	gca	cca	acc	ccc	gca	act	tat	gta	tca	ctg	ttt	787	
Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
	215					220					225						
aaa	gcg	att	ctt	cag	cgc	caa	gca	gac	acc	gtt	gga	aaa	tgg	acc	agg	835	
Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
230				235					240					245			
ctg	ggt	ttc	gtt	cac	gga	gcc	ctc	aac	aca	gac	aac	acg	ttg	ata	tcc	883	
Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250				255						260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265				270					275					
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggt	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		

295	300	305	
acc ctc ctc cca ctc ctg ggc gcc aca cca gac gaa ggc atg aca gca			1075
Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp Glu Gly Met Thr Ala			
310	315	320	325
gcc caa gaa gct ctc gta gaa ttc gat gac ctc tgc gaa caa gca atc			1123
Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu Cys Glu Gln Ala Ile			
	330	335	340
cga aaa gaa ttc gcc act gca ctg ggc ctt gac gag tca gac acc ggc			1171
Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp Glu Ser Asp Thr Gly			
	345	350	355
acg gta gag cag ttc cgt gaa ctg ctc tac ctc cat aac ccc gac atc			1219
Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu His Asn Pro Asp Ile			
	360	365	370
acc acg ctg ctg cgc gca ctc acc gac aac acc gca cca ccg agt ggc			1267
Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr Ala Pro Pro Ser Gly			
	375	380	385
ttt gaa gca ttc gtt cac gac tgg aaa acc caa gac cca gat atc gaa			1315
Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln Asp Pro Asp Ile Glu			
	395	400	405
gca atg cga gca gta aat cca ctt ttc att cca cgc aat cac ctc gtg			1363
Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro Arg Asn His Leu Val			
	410	415	420
gaa gct gct ctc gca gac gca gtt gaa ggg aat cta gaa aag ttc cac			1411
Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn Leu Glu Lys Phe His			
	425	430	435
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc			1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro			
	440	445	450
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg			1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met			
	455	460	465
acc ttc tgc ggt acc taggacagat ggtggggcag acg			1545
Thr Phe Cys Gly Thr			
470			

<210> 532

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

Met	Asn	Thr	Ala	Pro	Phe	Lys	Leu	Glu	Ala	Asp	Phe	Ala	Ser	Ala	Leu
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Pro	Thr	Met	Ala	Ala	Pro	Trp	Gln	Gly	Glu	Glu	Ala	Pro	Asn	Pro	Glu
			20					25					30		

Leu	Val	Ile	Leu	Asn	Asp	Asp	Leu	Ala	Tyr	Ser	Leu	Gly	Leu	Asp	Pro
	35						40					45			

Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn
 50 55 60
 Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln
 65 70 75 80
 Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu
 85 90 95
 Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys
 100 105 110
 Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val
 115 120 125
 Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala
 130 135 140
 Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg
 145 150 155 160
 Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val
 165 170 175
 Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser
 180 185 190
 Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
 195 200 205
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
 210 215 220
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
 225 230 235 240
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
 245 250 255
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
 260 265 270
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
 275 280 285
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
 290 295 300
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
 305 310 315 320
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
 325 330 335
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
 340 345 350
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
 355 360 365

His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
 370 375 380

Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
 385 390 395 400

Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
 405 410 415

Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430

Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445

Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460

Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

<210> 533
 <211> 1236
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1213)
 <223> RXC01703

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cgcgagggtt tgggggtctgc ctcgaacaaa tcttggggtt gtg gca tgg cca tcc 115
 Val Ala Trp Pro Ser
 1 5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg 163
 Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
 10 15 20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag 211
 His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
 25 30 35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc 259
 Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
 40 45 50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg 307
 Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
 55 60 65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca 355
 Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
 70 75 80 85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat 403
 Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp

90									95				100					
tcc Ser	ctt Leu	act Thr	ggt Gly 105	gtg Val	ctg Leu	ccg Pro	tgg Trp	cgt Arg 110	tcc Ser	ggc Gly	gaa Glu	acc Thr	ttc Phe 115	tac Tyr	aac Asn	451		
ggt Val	ccc Pro	tcc Ser 120	aac Asn	ggt Gly	cct Pro	gct Ala	gcg Ala 125	atc Ile	atg Met	atg Met	gcc Ala	cgc Arg 130	acc Thr	gac Asp	cgt Arg	499		
ttg Leu	gac Asp 135	gag Glu	gct Ala	atg Met	aaa Lys 140	atc Ile	acc Thr	gat Asp	tgg Trp	att Ile	ttt Phe 145	gac Asp	aac Asn	ctg Leu	atc Ile	547		
gat Asp 150	ggc Gly	gac Asp	ggc Gly	ctt Leu	gtg Val 155	atg Met	gac Asp	gga Gly	ttg Leu	cgc Arg 160	atg Met	cgc Arg	atg Met	cac His	gga Gly 165	595		
cct Pro	gag Glu	ctt Leu	gtc Val 170	cgt Arg	tcc Ser	atc Ile	cac His	ccg Pro	tat Tyr 175	tgc Cys	caa Gln	ggg Gly	gtc Val 180	gcc Ala	att Ile	643		
ggg Gly	gac Asp	ggc Gly	ctt Leu	gtg Val	gat Asp	cac His	tgg Trp 205	tcg Ser	gat Asp	gcc Ala	gat Asp	aag Lys 210	gca Ala	gaa Glu	gac Asp	739		
tcc Ser	ctc Leu 215	aaa Lys	tac Tyr	ttt Phe	gca Ala	cac His 220	atc Ile	cac His	gct Ala	gtg Val 225	ggt Val	cag Gln	gct Ala	gtg Val	tcg Ser	787		
cgg Arg 230	aag Lys	atg Met	acc Thr	aac Asn	ttc Phe 235	cac His	ggc Gly	gtt Val	att Ile	gat Asp 240	tgg Trp	gac Asp	acc Thr	ggg Gly	gac Asp 245	835		
ggc Gly	gac Asp	ggc Gly	ggt Gly	ttg Leu 250	ttc Phe	aag Lys	ggc Gly	att Ile 255	ttg Leu	gtc Val	cgc Arg	tat Tyr	tta Leu	gct Ala 260	gat Asp	883		
gtg Val	gcc Ala	atc Ile	cgc Arg 265	ctg Leu	cct Pro	gac Asp	gat Asp	tca Ser 270	cca Pro	acc Thr	aac Asn	cgg Arg	gaa Glu 275	acc Thr	aaa Lys	931		
aag Lys	att Ile	gca Ala 280	gca Ala	cgc Arg	ctg Leu	gta Val	ctg Leu 285	gaa Glu	tcg Ser	gcg Ala	gaa Glu	agc Ser 290	gta Val	tgg Trp	aac Asn	979		
cac His	cga Arg 295	ttg Leu	gaa Glu	gtt Val	gat Asp	ggc Gly 300	ctt Leu	ccg Pro	gta Val	ttc Phe	gcc Ala 305	aca Thr	gac Asp	tgg Trp	aca Thr	1027		
acg Thr 310	gat Asp	gca Ala	cgc Arg	ctg Leu	cca Pro	caa Gln	aac Asn	ttt Phe	ggg Gly	ttg Leu 320	agt Ser	tcc Ser	tct Ser	agt Ser	ttg Leu 325	1075		
agc Ser	gat Asp	ctg Leu	gtg Val	agt Ser	gtt Val	gtg Val	cgc Arg	gtg Val	gat Asp 335	gaa Glu	cgt Arg	gat Asp	ctg Leu	tcc Ser	gtg Val 340	1123		

caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa 1171
 Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu
 345 350 355

gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga 1213
 Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg
 360 365 370

tagccccgat agtgtatgtg ctg 1236

<210> 534

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Trp Pro Ser Asn Ala Lys Glu Lys Leu Phe Ile His Trp His
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Tyr Trp Trp Gln Ala His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg
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Arg Arg Thr Thr Lys Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg
 35 40 45

Gly Ile Ser Val Arg Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr
 50 55 60

Asp Asp Lys Ala Trp Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val
 65 70 75 80

Arg Lys Val Arg Thr Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile
 85 90 95

Val Asp Gly Ile Asp Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly
 100 105 110

Glu Thr Phe Tyr Asn Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met
 115 120 125

Ala Arg Thr Asp Arg Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile
 130 135 140

Phe Asp Asn Leu Ile Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg
 145 150 155 160

Met Arg Met His Gly Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys
 165 170 175

Gln Gly Val Ala Ile Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg
 180 185 190

Glu Arg Ala Gly Leu Thr Thr Thr Val Val Asp His Trp Ser Asp Ala
 195 200 205

Asp Lys Ala Glu Asp Ser Leu Lys Tyr Phe Ala His Ile His Ala Val
 210 215 220

Val Gln Ala Val Ser Arg Lys Met Thr Asn Phe His Gly Val Ile Asp

225	230	235	240
Trp Asp Thr Gly	Asp Gly Asp Gly Gly	Leu Phe Lys Gly	Ile Leu Val
	245	250	255
Arg Tyr Leu Ala	Asp Val Ala Ile	Arg Leu Pro Asp	Asp Ser Pro Thr
	260	265	270
Asn Arg Glu Thr	Lys Lys Ile Ala	Ala Arg Leu Val	Leu Glu Ser Ala
	275	280	285
Glu Ser Val Trp	Asn His Arg Leu	Glu Val Asp Gly	Leu Pro Val Phe
	290	295	300
Ala Thr Asp Trp	Thr Thr Asp Ala	Arg Leu Pro Gln	Asn Phe Gly Leu
305	310	315	320
Ser Ser Ser Ser	Leu Ser Asp Leu	Val Ser Val Val	Arg Val Asp Glu
	325	330	335
Arg Asp Leu Ser	Val Gln Leu Ser	Gly Trp Met Leu	Met Glu Ala Ala
	340	345	350
Ala Lys Val Ala	Glu Glu Leu Glu	Asn Asn Gly Asn	Ser Tyr Thr Gly
	355	360	365
Arg Ser Arg			
370			

<210> 535

<211> 800

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXC02254

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1	5	10	15	

cgc ttc ggt gga	cat ggt gcg cta	gct ggt cac gcc	ttg gga aac ctc	96
Arg Phe Gly Gly	Gly His Gly Ala	Leu Ala Gly His	Ala Leu Gly Asn	
20	25	30		

gtg atc gcg gcg	ttg acc gac att	ttg ggc acc tcc	cag cat gcg ctt	144
Val Ile Ala Ala	Leu Thr Asp Ile	Leu Gly Thr Ser	Gln His Ala Leu	
35	40	45		

gat caa atc gct	caa ctc gct gga	gcc aaa gga cgc	atc atc ccg gta	192
Asp Gln Ile Ala	Gln Leu Ala Gly	Ala Lys Gly Arg	Ile Ile Pro Val	
50	55	60		

tgt gct gaa cct	ttg gat ctt gaa	gcg gaa gta tca	ggc cta gac tct	240
Cys Ala Glu Pro	Leu Asp Leu Glu	Ala Glu Val Ser	Gly Leu Asp Ser	
65	70	75	80	

gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288
Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
85 90 95

acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336
Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
100 105 110

ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384
Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
115 120 125

ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432
Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
130 135 140

cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480
Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
145 150 155 160

gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528
Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
165 170 175

gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576
Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
180 185 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
195 200 205

aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
210 215 220

cat gat gtc cag gct gaa gat ggc cgt ggt cga ttc acc agt att cac 720
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
225 230 235 240

gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
245 250 255

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Arg Lys Arg

<210> 536

<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 536

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Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
20 25 30

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                               Val Ala Lys Asn Ser

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	1	5	
gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg			163
Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met			
	10	15	20
caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg			211
Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met			
	25	30	35
caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct			259
Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser			
	40	45	50
cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca			307
Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro			
	55	60	65
cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc			355
Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg			
	70	75	80
acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct			403
Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro			
	90	95	100
tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt			451
Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly			
	105	110	115
gcg ttt cta gcc aat gga tct tta agt gat cca ggt cgt tcc tct tcg			499
Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro Gly Arg Ser Ser Ser			
	120	125	130
ttg gag gtg ttg tgt cct ggt caa gaa tca gca ttg gca ctg gtt gga			547
Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala Leu Ala Leu Val Gly			
	135	140	145
tgt gcg cga aga att ggg atc gcg gcg aaa acg aaa gat tct cga gga			595
Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr Lys Asp Ser Arg Gly			
	150	155	160
ttt gat cgc gtc aat gtt cgt gat gcg gaa gca att ggg gca ctg ctc			643
Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala Ile Gly Ala Leu Leu			
	170	175	180
act cga atg ggt gcc cag aaa act cgc atg ttg tgg gaa gaa aaa cgc			691
Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu Trp Glu Glu Lys Arg			
	185	190	195
atc aag cgg gaa agt cga act ccg caa acc ggg ttg gcc aac ttc gac			739
Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly Leu Ala Asn Phe Asp			
	200	205	210
gat gcc aat ctg cgc agg tca gcc cga gca gca gtt gcc gct gca gcg			787
Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala Val Ala Ala Ala Ala			
	215	220	225
agg gta gaa cgc gcc atg aag att ctt ggt gat gat gtt cct gag cat			835
Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp Asp Val Pro Glu His			
	230	235	240
			245

ttg gct gag gct gga cag ctg cgt gtg cag cac cgt cag gca tcg ttg 883
 Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His Arg Gln Ala Ser Leu
 250 255 260
 gag gag ttg ggc cgg ttg gct gat cct caa atg acc aag gat gct gtg 931
 Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met Thr Lys Asp Ala Val
 265 270 275
 gcc ggt cgt att cgt cgt ctt ttg acg atg gca gat aag cgc gcc gaa 979
 Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala Asp Lys Arg Ala Glu
 280 285 290
 gat ctg aag att cct gat aca aat tct gtt gtg acg gaa gat ttg ttg 1027
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 gaa gaa att tagatgattg aagcctaaaa acg 1059
 Glu Glu Ile
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 <213> *Corynebacterium glutamicum*

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 20 25 30
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 35 40 45
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
 50 55 60
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65 70 75 80
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
 85 90 95
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
 100 105 110
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
 115 120 125
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
 130 135 140
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
 145 150 155 160
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
 165 170 175

Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
 180 185 190

Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
 195 200 205

Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
 210 215 220

Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
 225 230 235 240

Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
 245 250 255

Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
 260 265 270

Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
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 <223> RXC02435

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 Val Thr Asp Asn Leu
 1 5

ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
 10 15 20

gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35

cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
 40 45 50

ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65

atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70 75 80 85
 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
 90 95 100
 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
 105 110 115
 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499
 Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
 120 125 130
 acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
 135 140 145
 tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
 150 155 160 165
 att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Ala Ala Val Ile Leu
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 gga att gac cgg gtg tagacacatt ccgcccattg ccc 681
 Gly Ile Asp Arg Val
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<213> Corynebacterium glutamicum

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 Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
 35 40 45
 Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
 50 55 60
 Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65 70 75 80
 Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95
 Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
 100 105 110
 Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala

115	120	125
Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly		
130	135	140
Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr		
145	150	155
Gln Arg Thr Arg Trp Ile Ile Val Leu Ile Gly Phe Ala Val Val Val		
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Ala Ala Val Ile Leu Gly Ile Asp Arg Val		
180	185	

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 Val Thr Asp Asn Leu
 1 5

 ggt tca acc agt atc ggt gac gcg tgg att ctg tac gca ccg ctg atg 163
 Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu Tyr Ala Pro Leu Met
 10 15 20

 gat gat ggt ggc ttt ggt cca ctg cgt gcc atc gga gga atg ttc ctg 211
 Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile Gly Gly Met Phe Leu
 25 30 35

 cac att ggc ccc ggg cac atg ctg ttg aac ctt gtg ttg ttg tgg ttg 259
 His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
 40 45 50

 ctg gga aga gaa att gaa cga gac ttc ggt tct gcg ctt ttc act gcg 307
 Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser Ala Leu Phe Thr Ala
 55 60 65

 atg tac ttt gtg ggc ggt att ggt gcg tct gca gct gtc atc tgg atg 355
 Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala Ala Val Ile Trp Met
 70 75 80 85

 gat ccc tat tca ccg aca gca ggt gct tcc ggc gcc att tac gcc atg 403
 Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly Ala Ile Tyr Ala Met
 90 95 100

 atg gct att ttg gtg ggg ctt ttt gtg tta aga agc gcg gat atc cga 451
 Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg Ser Ala Asp Ile Arg
 105 110 115

 gca ccc ttg atc ctt atc gcc atc aac atc gcc tat acc ttg atg tcc 499

Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
 120 125 130

acc aat gtt tct ctg tgg gga cac ctt gga ggt ttg atc act gga gct 547
 Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
 135 140 145

tta att act tgg cca atg gtt aaa gcg aaa act caa aga aca cgg tgg 595
 Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp
 150 155 160 165

att atc gtg ctc att ggt ttt gct gta gtt gtg gct gct gtc att cta 643
 Ile Ile Val Leu Ile Gly Phe Ala Val Val Val Ala Ala Val Ile Leu
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gga att gac cgg gtg tagacacatt cgcgccattg ccc 681
 Gly Ile Asp Arg Val
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 Val Thr Asp Asn Leu Gly Ser Thr Ser Ile Gly Asp Ala Trp Ile Leu
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Tyr Ala Pro Leu Met Asp Asp Gly Gly Phe Gly Pro Leu Arg Ala Ile
 20 25 30

Gly Gly Met Phe Leu His Ile Gly Pro Gly His Met Leu Leu Asn Leu
 35 40 45

Val Leu Leu Trp Leu Leu Gly Arg Glu Ile Glu Arg Asp Phe Gly Ser
 50 55 60

Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
 65 70 75 80

Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95

Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
 100 105 110

Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
 115 120 125

Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
 130 135 140

Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
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Met Lys Leu Gly Leu																5
tac aac gcg atc ttc cac gac cgc acc ctg cca gaa gcg ctc gca gcc																163
Tyr Asn Ala Ile Phe His Asp Arg Thr Leu Pro Glu Ala Leu Ala Ala																20
atc aaa gct gca ggt ctc acc gga att gaa ctc aac acc ggc gga ttt																211
Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe																35
ttg cct gca acc cac atc ccg acc atc gat gac atc ctg gtc agc gat																259
Leu Pro Ala Thr His Ile Pro Thr Ile Asp Asp Ile Leu Val Ser Asp																50
gat gcc cgc gat gaa ttc ctc ggg att ttc gaa ggc acc ggc gtc gac																307
Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu Gly Thr Gly Val Asp																65
atc tac ggc ctt aac tgc aac ggc aac ccg ctt cac ccc aac aag gcg																355
Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu His Pro Asn Lys Ala																85
atc ggg gac aag cat gcc gaa gac att cga cgt tcc atc cgc ctc gca																403
Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg Ser Ile Arg Leu Ala																100
gag cgc ctc ggc caa aac cgt gtg gtc acc atg tct ggt ctt cct ggt																451
Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met Ser Gly Leu Pro Gly																115
ggc gaa cca ggc gcg aag tac acc aac tgg gtt gtc aac gcg tgg aac																499
Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val Val Asn Ala Trp Asn																130
tcc gca gcc ttg gat gtc ctt gat tac caa tgg gat atc gca gct gaa																547
Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp Asp Ile Ala Ala Glu																145
ttc tgg cgc gag acc gac cgc ttc gcc gca gat cac ggc gtg aaa gtg																595
Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp His Gly Val Lys Val																165
gct ctt gag ctg cac cca cag aac atc gtg ttc aac tcc gct gac gtg																643
Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe Asn Ser Ala Asp Val																

	170	175	180	
cat aag ctc atc gat ctc acc ggc gcc acc cac gtg ggc gtc gaa ctg				691
His Lys Leu Ile Asp Leu Thr Gly Ala Thr His Val Gly Val Glu Leu				
	185	190	195	
gat gca tca cac ctg ttc tgg cag cag atg gac cca atc gct gtg att				739
Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp Pro Ile Ala Val Ile				
	200	205	210	
gat cac ctc ggc gag ctc atc ttc cac gcc gcc gcc aaa gac gtg cga				787
Asp His Leu Gly Glu Leu Ile Phe His Ala Ala Ala Lys Asp Val Arg				
	215	220	225	
gtt aat aag gaa tgg gct cag ctc aac ggt gtg ctg gac aac agc ttc				835
Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val Leu Asp Asn Ser Phe				
	230	235	240	245
cga cgc ctt gac cca tcc gaa aac cgc acc aac ttg ggc ggc gac gag				883
Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn Leu Gly Gly Asp Glu				
	250	255	260	
tgg gcg aat gaa tgg cca aag aac tct gct tgg gat ttc gtt gct ctg				931
Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp Asp Phe Val Ala Leu				
	265	270	275	
ggc cgc ggt cat gac gtt gct tac tgg acc gaa ttc ctc cgc gca ctt				979
Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu Phe Leu Arg Ala Leu				
	280	285	290	
cac cgc gtc gat cca aac atg ctg gtc aac atc gaa cac gag gat gtt				1027
His Arg Val Asp Pro Asn Met Leu Val Asn Ile Glu His Glu Asp Val				
	295	300	305	
tca ctc ggt cgc gaa gaa ggc gtc aac gaa gcc gct aag gtg ctg atc				1075
Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile				
	310	315	320	325
gag gcc aac aag gca ctc gaa gag tcc ctg gtt tct taaaaaaact				1121
Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val Ser				
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			20					25					30		

Asn	Thr	Gly	Gly	Phe	Leu	Pro	Ala	Thr	His	Ile	Pro	Thr	Ile	Asp	Asp
		35					40					45			

Ile	Leu	Val	Ser	Asp	Asp	Ala	Arg	Asp	Glu	Phe	Leu	Gly	Ile	Phe	Glu
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50 55 60
 Gly Thr Gly Val Asp Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu
 65 70 75 80
 His Pro Asn Lys Ala Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg
 85 90 95
 Ser Ile Arg Leu Ala Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met
 100 105 110
 Ser Gly Leu Pro Gly Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val
 115 120 125
 Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp
 130 135 140
 Asp Ile Ala Ala Glu Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp
 145 150 155 160
 His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe
 165 170 175
 Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His
 180 185 190
 Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp
 195 200 205
 Pro Ile Ala Val Ile Asp His Leu Gly Glu Leu Ile Phe His Ala Ala
 210 215 220
 Ala Lys Asp Val Arg Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val
 225 230 235 240
 Leu Asp Asn Ser Phe Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn
 245 250 255
 Leu Gly Gly Asp Glu Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp
 260 265 270
 Asp Phe Val Ala Leu Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu
 275 280 285
 Phe Leu Arg Ala Leu His Arg Val Asp Pro Asn Met Leu Val Asn Ile
 290 295 300
 Glu His Glu Asp Val Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala
 305 310 315 320
 Ala Lys Val Leu Ile Glu Ala Asn Lys Ala Leu Glu Glu Ser Leu Val
 325 330 335
 Ser

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<212> DNA

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<223> RXA02175

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Val Ala Thr Asp Asn
1 5

aac aag gct gtc ctg cac tac ccc ggt ggc gag ttc gaa atg gac atc 163
Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
10 15 20

atc gag gct tct gag ggt aac aac ggt gtt gtc ctg ggc aag atg ctg 211
Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
25 30 35

tct gag act gga ctg atc act ttt gac cca ggt tat gtg agc act ggc 259
Ser Glu Thr Gly Leu Ile Thr Phe Asp Pro Gly Tyr Val Ser Thr Gly
40 45 50

tcc acc gag tcg aag atc acc tac atc gat ggc gat gcg gga atc ctg 307
Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
55 60 65

cgt tac cgc ggc tat gac atc gct gat ctg gct gag aat gcc acc ttc 355
Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe
70 75 80 85

aac gag gtt tct tac cta ctt atc aac ggt gag cta cca acc cca gat 403
Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp
90 95 100

gag ctt cac aag ttt aac gac gag att cgc cac cac acc ctt ctg gac 451
Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp
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gag gac ttc aag tcc cag ttc aac gtg ttc cca cgc gac gct cac cca 499
Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro Arg Asp Ala His Pro
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atg gca acc ttg gct tcc tcg gtt aac att ttg tct acc tac tac cag 547
Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln
135 140 145

gac cag ctg aac cca ctc gat gag gca cag ctt gat aag gca acc gtt 595
Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val
150 155 160 165

cgc ctc atg gca aag gtt cca atg ctg gct gcg tac gca cac cgc gca 643
Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala
170 175 180

cgc aag ggt gct cct tac atg tac cca gac aac tcc ctc aat gcg cgt 691
Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg
185 190 195

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Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
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Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr Val Arg Met Ile Gly	
230 235 240 245	
tcc gca cag gcc aac atg ttt gtc tcc atc gct ggt ggc atc aac gct	883
Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
250 255 260	
ctg tcc ggc cca ctg cac ggt ggc gca aac cag gct gtt ctg gag atg	931
Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
265 270 275	
ctc gaa gac atc aag agc aac cac ggt ggc gac gca acc gag ttc atg	979
Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp Ala Thr Glu Phe Met	
280 285 290	
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Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
295 300 305	
cac cgc gtt tac aag aac tac gat cca cgt gca gca atc gtc aag gag	1075
His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala Ala Ile Val Lys Glu	
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Thr Ala His Glu Ile Leu Glu His Leu Gly Gly Asp Asp Leu Leu Asp	
330 335 340	
ctg gca atc aag ctg gaa gaa att gca ctg gct gat gat tac ttc atc	1171
Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala Asp Asp Tyr Phe Ile	
345 350 355	
tcc cgc aag ctc tac ccg aac gta gac ttc tac acc ggc ctg atc tac	1219
Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr Thr Gly Leu Ile Tyr	
360 365 370	
cgc gca atg ggc ttc cca act gac ttc ttc acc gta ttg ttc gca atc	1267
Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile	
375 380 385	
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Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg Glu Gln Leu Gly Ala	
390 395 400 405	
gca ggc aac aag atc aac cgc cca cgc cag gtc tac acc ggc aac gaa	1363
Ala Gly Asn Lys Ile Asn Arg Pro Arg Gln Val Tyr Thr Gly Asn Glu	
410 415 420	
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Ser Arg Lys Leu Val Pro Arg Glu Glu Arg	
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cgt	1416

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Phe	Glu	Met	Asp	Ile	Ile	Glu	Ala	Ser	Glu	Gly	Asn	Asn	Gly	Val	Val
			20					25					30		
Leu	Gly	Lys	Met	Leu	Ser	Glu	Thr	Gly	Leu	Ile	Thr	Phe	Asp	Pro	Gly
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Tyr	Val	Ser	Thr	Gly	Ser	Thr	Glu	Ser	Lys	Ile	Thr	Tyr	Ile	Asp	Gly
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Asp	Ala	Gly	Ile	Leu	Arg	Tyr	Arg	Gly	Tyr	Asp	Ile	Ala	Asp	Leu	Ala
65					70				75						80
Glu	Asn	Ala	Thr	Phe	Asn	Glu	Val	Ser	Tyr	Leu	Leu	Ile	Asn	Gly	Glu
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Leu	Pro	Thr	Pro	Asp	Glu	Leu	His	Lys	Phe	Asn	Asp	Glu	Ile	Arg	His
			100					105					110		
His	Thr	Leu	Leu	Asp	Glu	Asp	Phe	Lys	Ser	Gln	Phe	Asn	Val	Phe	Pro
	115						120					125			
Arg	Asp	Ala	His	Pro	Met	Ala	Thr	Leu	Ala	Ser	Ser	Val	Asn	Ile	Leu
	130					135					140				
Ser	Thr	Tyr	Tyr	Gln	Asp	Gln	Leu	Asn	Pro	Leu	Asp	Glu	Ala	Gln	Leu
145					150				155						160
Asp	Lys	Ala	Thr	Val	Arg	Leu	Met	Ala	Lys	Val	Pro	Met	Leu	Ala	Ala
				165					170					175	
Tyr	Ala	His	Arg	Ala	Arg	Lys	Gly	Ala	Pro	Tyr	Met	Tyr	Pro	Asp	Asn
		180					185						190		
Ser	Leu	Asn	Ala	Arg	Glu	Asn	Phe	Leu	Arg	Met	Met	Phe	Gly	Tyr	Pro
		195					200					205			
Thr	Glu	Pro	Tyr	Glu	Ile	Asp	Pro	Ile	Met	Val	Lys	Ala	Leu	Asp	Lys
	210					215					220				
Leu	Leu	Ile	Leu	His	Ala	Asp	His	Glu	Gln	Asn	Cys	Ser	Thr	Ser	Thr
225					230					235					240
Val	Arg	Met	Ile	Gly	Ser	Ala	Gln	Ala	Asn	Met	Phe	Val	Ser	Ile	Ala
				245					250					255	
Gly	Gly	Ile	Asn	Ala	Leu	Ser	Gly	Pro	Leu	His	Gly	Gly	Ala	Asn	Gln
			260				265						270		
Ala	Val	Leu	Glu	Met	Leu	Glu	Asp	Ile	Lys	Ser	Asn	His	Gly	Gly	Asp
		275					280					285			

Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg
 290 295 300

Leu Met Gly Phe Gly His Arg Val Tyr Lys Asn Tyr Asp Pro Arg Ala
 305 310 315 320

Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly
 325 330 335

Asp Asp Leu Leu Asp Leu Ala Ile Lys Leu Glu Glu Ile Ala Leu Ala
 340 345 350

Asp Asp Tyr Phe Ile Ser Arg Lys Leu Tyr Pro Asn Val Asp Phe Tyr
 355 360 365

Thr Gly Leu Ile Tyr Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr
 370 375 380

Val Leu Phe Ala Ile Gly Arg Leu Pro Gly Trp Ile Ala His Tyr Arg
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 Met Ser Glu Leu Ile
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tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163
 Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile
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 Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp
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 Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu
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tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307
 Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser
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gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc 355
Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe
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Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu
90 95 100

gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc 451
Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr
105 110 115

agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg 499
Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp
120 125 130

ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc 547
Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe
135 140 145

ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt 595
Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu
150 155 160 165

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Thr Arg Ala Leu Met His Leu His Ala Ala Ala Asn Gly Lys Phe Thr
170 175 180

att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta 691
Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu
185 190 195

gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att 739
Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile
200 205 210

cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct 787
His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala
215 220 225

aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat 835
Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His
230 235 240 245

cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att 883
Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile
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Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg
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Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val
 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser
 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr
 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val
 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly
 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg
 145 150 155 160

Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala
 165 170 175

Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu
 180 185 190

Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala
 195 200 205

Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala
 210 215 220

Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu
 225 230 235 240

Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile
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Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro
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Ala

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<213> Corynebacterium glutamicum

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				Met	Ala	Lys	Ile	Ile		
				1				5		

tgg	acc	cgc	acc	gac	gaa	gca	ccg	ctg	ctc	gcg	acc	tac	tcg	ctg	aag	163
Trp	Thr	Arg	Thr	Asp	Glu	Ala	Pro	Leu	Leu	Ala	Thr	Tyr	Ser	Leu	Lys	
				10				15						20		

ccg	gtc	gtc	gag	gca	ttt	gct	gct	acc	gcg	ggc	att	gag	gtc	gag	acc	211
Pro	Val	Val	Glu	Ala	Phe	Ala	Ala	Thr	Ala	Gly	Ile	Glu	Val	Glu	Thr	
			25					30					35			

cgg	gac	att	tca	ctc	gct	gga	cgc	atc	ctc	gcc	cag	ttc	cca	gag	cgc	259
Arg	Asp	Ile	Ser	Leu	Ala	Gly	Arg	Ile	Leu	Ala	Gln	Phe	Pro	Glu	Arg	
		40					45					50				

ctc	acc	gaa	gat	cag	aag	gta	ggc	aac	gca	ctc	gca	gaa	ctc	ggc	gag	307
Leu	Thr	Glu	Asp	Gln	Lys	Val	Gly	Asn	Ala	Leu	Ala	Glu	Leu	Gly	Glu	
		55				60					65					

ctt	gct	aag	act	cct	gaa	gca	aac	atc	att	aag	ctt	cca	aac	atc	tcc	355
Leu	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Ile	Ile	Lys	Leu	Pro	Asn	Ile	Ser	
	70				75					80				85		

gct	tct	gtt	cca	cag	ctc	aag	gct	gct	att	aag	gaa	ctg	cag	gac	cag	403
Ala	Ser	Val	Pro	Gln	Leu	Lys	Ala	Ala	Ile	Lys	Glu	Leu	Gln	Asp	Gln	
				90					95					100		

ggc	tac	gac	atc	cca	gaa	ctg	cct	gat	aac	gcc	acc	acc	gac	gag	gaa	451
Gly	Tyr	Asp	Ile	Pro	Glu	Leu	Pro	Asp	Asn	Ala	Thr	Thr	Asp	Glu	Glu	
			105					110					115			

aaa	gac	atc	ctc	gca	cgc	tac	aac	gct	gtt	aag	ggc	tcc	gct	gtg	aac	499
Lys	Asp	Ile	Leu	Ala	Arg	Tyr	Asn	Ala	Val	Lys	Gly	Ser	Ala	Val	Asn	
		120					125					130				

cca	gtg	ctg	cgt	gaa	ggc	aac	tct	gac	cgc	cgc	gca	cca	atc	gct	gtc	547
Pro	Val	Leu	Arg	Glu	Gly	Asn	Ser	Asp	Arg	Arg	Ala	Pro	Ile	Ala	Val	
	135					140					145					

aag	aac	ttt	gtt	aag	aag	ttc	cca	cac	cgc	atg	ggc	gag	tgg	tct	gca	595
Lys	Asn	Phe	Val	Lys	Lys	Phe	Pro	His	Arg	Met	Gly	Glu	Trp	Ser	Ala	
	150				155					160					165	

gat	tcc	aag	acc	aac	gtt	gca	acc	atg	gat	gca	aac	gac	ttc	cgc	cac	643
Asp	Ser	Lys	Thr	Asn	Val	Ala	Thr	Met	Asp	Ala	Asn	Asp	Phe	Arg	His	
				170					175					180		

aac	gag	aag	tcc	atc	atc	ctc	gac	gct	gct	gat	gaa	gtt	cag	atc	aag	691
Asn	Glu	Lys	Ser	Ile	Ile	Leu	Asp	Ala	Ala	Asp	Glu	Val	Gln	Ile	Lys	
			185					190					195			

cac	atc	gca	gct	gac	ggc	acc	gag	acc	atc	ctc	aag	gac	agc	ctc	aag	739
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His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys	
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ctt ctt gaa ggc gaa gtt cta gac gga acc gtt ctg tcc gca aag gca	787
Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala	
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Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly	
230 235 240 245	
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Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp	
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Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe	
265 270 275	
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Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn	
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Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu	
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Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu	
310 315 320 325	
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Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn Leu His Val Pro Ser	
330 335 340	
gat gtc atc gtg gac gct tcc atg cca gca atg att cgt acc tcc ggc	1171
Asp Val Ile Val Asp Ala Ser Met Pro Ala Met Ile Arg Thr Ser Gly	
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cac atg tgg aac aaa gac gac cag gag cag gac acc ctg gca atc atc	1219
His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile	
360 365 370	
cca gac tcc tcc tac gct ggc gtc tac cag acc gtt atc gaa gac tgc	1267
Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr Val Ile Glu Asp Cys	
375 380 385	
cgc aag aac ggc gca ttc gat cca acc acc atg ggt acc gtc cct aac	1315
Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met Gly Thr Val Pro Asn	
390 395 400 405	
gtt ggt ctg atg gct cag aag gct gaa gag tac ggc tcc cat gac aag	1363
Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr Gly Ser His Asp Lys	
410 415 420	
acc ttc cgc atc gaa gca gac ggt gtg gtt cag gtt gtt tcc tcc aac	1411
Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln Val Val Ser Ser Asn	
425 430 435	
ggc gac gtt ctc atc gag cac gac gtt gag gca aat gac atc tgg cgt	1459
Gly Asp Val Leu Ile Glu His Asp Val Glu Ala Asn Asp Ile Trp Arg	

440	445	450	
gca tgc cag gtc aag gat gcc cca atc cag gat tgg gta aag ctt gct			1507
Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp Trp Val Lys Leu Ala			
455	460	465	
gtc acc cgc tcc cgt ctc tcc gga atg cct gca gtg ttc tgg ttg gat			1555
Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala Val Phe Trp Leu Asp			
470	475	480	485
cca gag cgc gca cac gac cgc aac ctg gct tcc ctc gtt gag aag tac			1603
Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr			
	490	495	500
ctg gct gac cac gac acc gag ggc ctg gac atc cag atc ctc tcc cct			1651
Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile Gln Ile Leu Ser Pro			
	505	510	515
gtt gag gca acc cag ctc tcc atc gac cgc atc cgc cgt ggc gag gac			1699
Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp			
	520	525	530
acc atc tct gtc acc ggt aac gtt ctg cgt gac tac aac acc gac ctc			1747
Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp Tyr Asn Thr Asp Leu			
	535	540	545
ttc cca atc ctg gag ctg ggc acc tct gca aag atg ctg tct gtc gtt			1795
Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys Met Leu Ser Val Val			
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cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct			1843
Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser			
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gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg			1891
Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp			
	585	590	595
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag			1939
Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu			
	600	605	610
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg			1987
Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu			
	615	620	625
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc			2035
Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg			
630	635	640	645
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag			2083
Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys			
	650	655	660
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct			2131
Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala			
	665	670	675
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac			2179
Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp			
	680	685	690

atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt 2227
 Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly
 695 700 705

ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca 2275
 Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro
 710 715 720 725

gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct 2324
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tcacaaaaag cgc 2337

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 35 40 45

Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
 50 55 60

Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80

Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
 85 90 95

Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
 100 105 110

Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
 115 120 125

Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
 130 135 140

Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
 145 150 155 160

Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
 165 170 175

Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
 180 185 190

Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu
 195 200 205

Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val
 210 215 220
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg
 225 230 235 240
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met
 245 250 255
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr
 260 265 270
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly
 275 280 285
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser
 290 295 300
 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu
 305 310 315 320
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn
 325 330 335
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
 340 345 350
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp
 355 360 365
 Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr
 370 375 380
 Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met
 385 390 395 400
 Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr
 405 410 415
 Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln
 420 425 430
 Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala
 435 440 445
 Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp
 450 455 460
 Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala
 465 470 475 480
 Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser
 485 490 495
 Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile
 500 505 510
 Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile
 515 520 525
 Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp

530 535 540
 Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys
 545 550 555 560
 Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr
 565 570 575
 Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu
 580 585 590
 Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu
 595 600 605
 Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val
 610 615 620
 Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu
 625 630 635 640
 Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His
 645 650 655
 Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu
 660 665 670
 Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn
 675 680 685
 Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly
 690 695 700
 Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr
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Lys Lys

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 <223> FRXA00521

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 acc gag acc atc ctc aag gac agc ctc aag ctt ctt gaa ggc gaa gtt 96
 Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val
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cta gac gga acc gtt ctg tcc gca aag gca ctg gac gca ttc ctt ctc	144
Leu Asp Gly Thr Val Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu	
35 40 45	
gag cag gtc gct cgc gca aag gca gaa ggt atc ctc ttc tcc gca cac	192
Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His	
50 55 60	
ctg aag gcc acc atg atg aag gtc tcc gac cca atc atc ttc ggc cac	240
Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His	
65 70 75 80	
gtt gtg cgc gct tac ttc gca gac gtt ttc gca cag tac ggt gag cag	288
Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln	
85 90 95	
ctg ctc gca gct ggc ctc aac ggc gaa aac ggc ctc gct gca atc ctc	336
Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu	
100 105 110	
tcc ggc ttg gag tcc ctg gac aac ggc gaa gaa atc aag gct gca ttc	384
Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe	
115 120 125	
gag aag ggc ttg gaa gac ggc cca gac ctg gcc atg gtt aac tcc gct	432
Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala	
130 135 140	
cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
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aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864

Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
 275 280 285

tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac 912
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
 290 295 300

cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc 960
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
 305 310 315 320

gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc 1008
 Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
 325 330 335

tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt 1056
 Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
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 <213> Corynebacterium glutamicum

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 35 40 45

Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
 50 55 60

Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
 65 70 75 80

Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
 85 90 95

Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
 100 105 110

Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
 115 120 125

Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
 130 135 140

Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
 145 150 155 160

Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp

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Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	Arg	Lys	Asn	Gly	Ala	Phe				
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Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	Thr	Phe	Arg	Ile	Glu	Ala				
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His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	Ala	Cys	Gln	Val	Lys	Asp				
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Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala	Val	Thr	Arg	Ser	Arg	Leu				
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Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp	Pro	Glu	Arg	Ala	His	Asp				
	290					295					300								
Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr	Leu	Ala	Asp	His	Asp	Thr				
305					310					315					320				
Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Tyr	Pro	Val	Glu	Ala	Thr	Gln	Leu				
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Asn

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 <223> RXN02209

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gac cgc atc ctt ctc tcc gag gca aag gag cag ttc cgt aag gat ctg															96	
Asp	Arg	Ile	Leu	Leu	Ser	Glu	Ala	Lys	Glu	Gln	Phe	Arg	Lys	Asp	Leu	
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cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca															144	
Pro	Thr	Tyr	Thr	Asp	Asp	Ala	Val	Ser	Val	Asp	Thr	Ser	Ile	Pro	Ala	
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Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu	
50 55 60	
gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct	240
Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala	
65 70 75 80	
act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca	288
Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro	
85 90 95	
cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc	336
Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser	
100 105 110	
atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct	384
Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala	
115 120 125	
ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct	432
Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro	
130 135 140	
tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac	480
Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr	
145 150 155 160	
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Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg	576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
195 200 205	
gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	

gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
305 310 315 320	
tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
385 390 395 400	
ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca	1248
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala	
405 410 415	
ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc	1296
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe	
420 425 430	
atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc	1344
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val	
435 440 445	
gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca	1392
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala	
450 455 460	
gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc	1440
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser	
465 470 475 480	
ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca	1488
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro	
485 490 495	
ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc	1536
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly	
500 505 510	
acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag	1584
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu	
515 520 525	
act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc	1632

Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
 530 535 540
 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
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 tactaccgcc acg 1694

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 Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
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 Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65 70 75 80
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
 85 90 95
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
 100 105 110
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
 115 120 125
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
 130 135 140
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
 145 150 155 160
 Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
 165 170 175
 Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
 180 185 190
 Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
 195 200 205
 Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
 210 215 220
 Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
 225 230 235 240

Ile	Ala	Gly	Thr	Met	Asp	Phe	Asp	Phe	Glu	Asn	Glu	Ala	Leu	Gly	Gln
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Asp	Gln	Asp	Gly	Asn	Asp	Val	Phe	Leu	Lys	Asp	Ile	Trp	Pro	Ser	Thr
			260					265					270		
Glu	Glu	Ile	Glu	Asp	Thr	Ile	Gln	Gln	Ala	Ile	Ser	Arg	Glu	Leu	Tyr
		275					280					285			
Glu	Ala	Asp	Tyr	Ala	Asp	Val	Phe	Lys	Gly	Asp	Lys	Gln	Trp	Gln	Glu
	290					295					300				
Leu	Asp	Val	Pro	Thr	Gly	Asp	Thr	Phe	Glu	Trp	Asp	Glu	Asn	Ser	Thr
305					310					315					320
Tyr	Ile	Arg	Lys	Ala	Pro	Tyr	Phe	Asp	Gly	Met	Pro	Val	Glu	Pro	Val
				325					330					335	
Ala	Val	Thr	Asp	Ile	Gln	Gly	Ala	Arg	Val	Leu	Ala	Lys	Leu	Gly	Asp
			340					345					350		
Ser	Val	Thr	Thr	Asp	His	Ile	Ser	Pro	Ala	Ser	Ser	Ile	Lys	Pro	Gly
	355						360					365			
Thr	Pro	Ala	Ala	Gln	Tyr	Leu	Asp	Glu	His	Gly	Val	Glu	Arg	His	Asp
	370					375					380				
Tyr	Asn	Ser	Leu	Gly	Ser	Arg	Arg	Gly	Asn	His	Glu	Val	Met	Met	Arg
385					390					395					400
Gly	Thr	Phe	Ala	Asn	Ile	Arg	Leu	Gln	Asn	Gln	Leu	Val	Asp	Ile	Ala
				405					410					415	
Gly	Gly	Tyr	Thr	Arg	Asp	Phe	Thr	Gln	Glu	Gly	Ala	Pro	Gln	Ala	Phe
			420					425					430		
Ile	Tyr	Asp	Ala	Ser	Val	Asn	Tyr	Lys	Ala	Ala	Gly	Ile	Pro	Leu	Val
	435						440					445			
Val	Leu	Gly	Gly	Lys	Glu	Tyr	Gly	Thr	Gly	Ser	Ser	Arg	Asp	Trp	Ala
	450					455					460				
Ala	Lys	Gly	Thr	Asn	Leu	Leu	Gly	Ile	Arg	Ala	Val	Ile	Thr	Glu	Ser
465					470					475					480
Phe	Glu	Arg	Ile	His	Arg	Ser	Asn	Leu	Ile	Gly	Met	Gly	Val	Val	Pro
				485					490					495	
Leu	Gln	Phe	Pro	Ala	Gly	Glu	Ser	His	Glu	Ser	Leu	Gly	Leu	Asp	Gly
			500					505					510		
Thr	Glu	Thr	Phe	Asp	Ile	Thr	Gly	Leu	Thr	Ala	Leu	Asn	Glu	Gly	Glu
	515						520					525			
Thr	Pro	Lys	Thr	Val	Lys	Val	Thr	Ala	Thr	Lys	Glu	Asn	Gly	Asp	Val
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Val	Glu	Phe	Asp	Ala	Ile	Cys	Pro	His	Arg	His	Pro	Arg			
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 <223> FRXA02209

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 ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc 96
 Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
 20 25 30
 gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt 144
 Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
 35 40 45
 aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac 192
 Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
 50 55 60
 aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa 240
 Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
 65 70 75 80
 gga cgt cct tcc aag cca gtc acc gtt gca tcc cca cag ggt ggc gag 288
 Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
 85 90 95
 tac acc atc gac cac ggc atg gtt gca att gca tcc atc acc tct tgc 336
 Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
 100 105 110
 acc aac acc tct aac cca tcc gtg atg atc ggc gct ggc ctg atc gca 384
 Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
 115 120 125
 cgt aag gca gca gaa aag ggc ctc aag tcc aag cct tgg gtt aag acc 432
 Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac tac cag cgc gca 480
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac ctc tcc ggc ttc 528
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg cca gag gaa atc 576
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 tcc gct gcg atc aac gag cac gac ctg acc gca acc gca gtt ttg tcc 624
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser

195	200	205	
ggt aac cgt aac ttc gag gga cgt atc tcc cct gac gtt aag atg aac Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn 210 215 220			672
tac ctg gca tcc cca atc atg gtc att gct tac gca atc gct ggc acc Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr 225 230 235 240			720
atg gac ttc gac ttc gag aac gaa gct ctt gga cag gac cag gac ggc Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly 245 250 255			768
aac gac gtc ttc ctg aag gac atc tgg cct tcc acc gag gaa atc gaa Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu 260 265 270			816
gac acc atc cag cag gca atc tcc cgt gag ctt tac gaa gct gac tac Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr 275 280 285			864
gca gat gtc ttc aag ggt gac aag cag tgg cag gaa ctc gat gtt cct Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro 290 295 300			912
acc ggt gac acc ttc gag tgg gac gag aac tcc acc tac atc cgc aag Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys 305 310 315 320			960
gca cct tac ttc gac ggc atg cct gtc gag cca gtg gca gtc acc gac Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp 325 330 335			1008
atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr 340 345 350			1056
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala 355 360 365			1104
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu 370 375 380			1152
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala 385 390 395 400			1200
aac atc cgc ctc cag aac cag ctg gtt gac atc gca ggt ggc tac acc Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr 405 410 415			1248
cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala 420 425 430			1296
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly 435 440 445			1344

aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act 1392
Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
450 455 460

aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att 1440
Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
465 470 475 480

cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct 1488
His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
485 490 495

gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc 1536
Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
500 505 510

gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act 1584
Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
515 520 525

gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac 1632
Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
530 535 540

gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc 1679
Ala Ile Cys Pro His Arg His Pro Arg
545 550

acg 1682

<210> 556
<211> 553
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 556
Val Val Pro Ser Ile Ala Gly Pro Lys Arg Pro Gln Asp Arg Ile Leu
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Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
20 25 30

Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
35 40 45

Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
50 55 60

Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
65 70 75 80

Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
85 90 95

Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
100 105 110

Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
115 120 125

Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
 195 200 205
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
 210 215 220
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
 225 230 235 240
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
 245 250 255
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
 260 265 270
 Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
 275 280 285
 Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
 290 295 300
 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
 305 310 315 320
 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
 325 330 335
 Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
 340 345 350
 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
 355 360 365
 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
 370 375 380
 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
 385 390 395 400
 Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
 405 410 415
 Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
 420 425 430
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
 435 440 445

Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
 450 455 460
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
 465 470 475 480
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
 485 490 495
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
 500 505 510
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
 515 520 525
 Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp
 530 535 540
 Ala Ile Cys Pro His Arg His Pro Arg
 545 550

<210> 557
 <211> 874
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXN02213

<400> 557
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 gcgaaatctc accctaaaaa agttagaatt ggagctcact gtg act gaa agc aag 115
 Val Thr Glu Ser Lys
 1 5
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
 10 15 20
 gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35
 tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50
 aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65
 tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85
 cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg

	90	95	100	
gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg				451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu				
	105	110	115	
aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc				499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe				
	120	125	130	
ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc				547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg				
	135	140	145	
aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc				595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser				
	150	155	160	165
aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac				643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn				
	170	175	180	
att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac				691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr				
	185	190	195	
cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc				739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly				
	200	205	210	
ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca				787
Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala				
	215	220	225	
atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc				835
Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe				
	230	235	240	245
aag ttg acc ggc gag atc cca gta ggc gtt acc gca act				874
Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr				
	250	255		

<210> 558

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val			
1	5	10	15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met			
20	25	30	

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg			
35	40	45	

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala			
50	55	60	

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80
 Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95
 Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110
 Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125
 Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140
 Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro
 225 230 235 240
 Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr
 245 250 255

Ala Thr

<210> 559
 <211> 817
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(817)
 <223> FRXA02213

<400> 559
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 Val Thr Glu Ser Lys
 1 5
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
 10 15 20

gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35

tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85

cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
 90 95 100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451
 Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
 105 110 115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499
 Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
 120 125 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547
 Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
 135 140 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595
 Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
 150 155 160 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643
 Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
 170 175 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691
 Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
 185 190 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739
 Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
 200 205 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca 787
 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
 215 220 225

atg ctc ggc cag cca gtg tcc atg ctg atc 817
 Met Leu Gly Gln Pro Val Ser Met Leu Ile
 230 235

<210> 560

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Thr Glu Ser Lys Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val
 1 5 10 15

Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
 20 25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
 35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
 50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220

Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile
 225 230 235

<210> 561

<211> 2891

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2868)

<223> RXA02056

<400> 561

cgc cac tct gtt cca cgt cta acc aag ggc cag ggc acc atc atc ggt 48
 Arg His Ser Val Pro Arg Leu Thr Lys Gly Gln Gly Thr Ile Ile Gly

1	5	10	15	
gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac	96			
Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp				
20 25 30				
cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc	144			
Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr				
35 40 45				
tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc	192			
Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg				
50 55 60				
acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc	240			
Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe				
65 70 75 80				
gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt	288			
Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val				
85 90 95				
cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag	336			
Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu				
100 105 110				
gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca	384			
Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser				
115 120 125				
tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc	432			
Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile				
130 135 140				
gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc	480			
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val				
145 150 155 160				
ggt ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc	528			
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser				
165 170 175				
cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac	576			
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His				
180 185 190				
atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc	624			
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala				
195 200 205				
gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag	672			
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys				
210 215 220				
ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc	720			
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val				
225 230 235 240				
ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg	768			
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu				
245 250 255				

atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt	816
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val	
260 265 270	
gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc	864
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile	
275 280 285	
gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg	912
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met	
290 295 300	
gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt	960
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly	
305 310 315 320	
tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc	1008
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val	
325 330 335	
tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg	1056
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met	
340 345 350	
gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac	1104
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp	
355 360 365	
ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca	1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	
370 375 380	
ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc	1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	
385 390 395 400	
tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc	1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
405 410 415	
ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac	1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	
420 425 430	
tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac	1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	
435 440 445	
cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt	1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	
450 455 460	
cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc	1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	
465 470 475 480	
ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	

gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	
ggc ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg	1872
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu	
610 615 620	
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc	1920
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg	
625 630 635 640	
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct	1968
Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala	
645 650 655	
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac	2016
Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn	
660 665 670	
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg	2064
Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met	
675 680 685	
ggc ttc gag tac ggc tac tcc gta gga aac gaa gac tcc atc gtt gca	2112
Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala	
690 695 700	
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc	2160
Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile	
705 710 715 720	
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag	2208
Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys	
725 730 735	
ctg atc ctt ctg ctg cct cac ggc tac gaa ggc cag ggc cca gac cac	2256

Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His	
740 745 750	
tct tcc gca cgt atc gag cgc ttc ctg cag ctg tgc gct gag ggt tcc	2304
Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser	
755 760 765	
atg act gtt gct cag cca tcc acc cca gca aac cac ttc cac cta ctg	2352
Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu	
770 775 780	
cgt cgt cac gct ctg tcc gac ctg aag cgt cca ctg gtt atc ttc acc	2400
Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr	
785 790 795 800	
ccg aag tcc atg ctg cgt aac aag gct gct gcc tcc gca cca gaa gac	2448
Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ser Ala Pro Glu Asp	
805 810 815	
ttc act gag gtc acc aag ttc cag tcc gtg atc aac gat cca aac gtt	2496
Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val	
820 825 830	
gca gat gca gcc aag gtg aag aag gtc atg ctg gtc tcc ggc aag ctg	2544
Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu	
835 840 845	
tac tac gaa ttg gca aag cgc aag gag aag gac gga cgc gac gac atc	2592
Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile	
850 855 860	
gcg atc gtt cgt atc gaa atg ctc cac cca att ccg ttc aac cgc atc	2640
Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile	
865 870 875 880	
tcc gag gct ctt gcc ggc tac cct aac gct gag gaa gtc ctc ttc gtt	2688
Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val	
885 890 895	
cag gat gag cca gca aac cag ggc cca tgg ccg ttc tac cag gag cac	2736
Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His	
900 905 910	
ctc cca gag ctg atc ccg aac atg cca aag atg cgc cgc gtt tcc cgc	2784
Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg	
915 920 925	
cgc gct cag tcc tcc acc gca act ggt gtt gcc aag gtg cac cag ctg	2832
Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu	
930 935 940	
gag gag aag cag ctt atc gac gag gct ttc gag gct taagtcttta	2878
Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala	
945 950 955	
tagtcctgca cta	2891

<210> 562

<211> 956

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

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 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp
 20 25 30
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
 35 40 45
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
 50 55 60
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65 70 75 80
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
 85 90 95
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
 100 105 110
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
 115 120 125
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile
 130 135 140
 Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val
 145 150 155 160
 Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser
 165 170 175
 Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His
 180 185 190
 Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala
 195 200 205
 Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys
 210 215 220
 Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val
 225 230 235 240
 Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu
 245 250 255
 Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val
 260 265 270
 Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile
 275 280 285
 Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met
 290 295 300
 Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly

305		310		315		320
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val						
	325			330		335
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met						
	340			345		350
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp						
	355			360		365
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala						
	370			375		380
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly						
	385			390		395
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly						
	405			410		415
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp						
	420			425		430
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp						
	435			440		445
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg						
	450			455		460
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg						
	465			470		475
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr						
	485			490		495
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp						
	500			505		510
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val						
	515			520		525
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu						
	530			535		540
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln						
	545			550		555
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu						
	565			570		575
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His						
	580			585		590
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu						
	595			600		605
Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu						
	610			615		620
Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg						
	625			630		635
						640

Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
 645 650 655
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
 660 665 670
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
 675 680 685
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
 690 695 700
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
 705 710 715 720
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
 725 730 735
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
 740 745 750
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
 755 760 765
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
 770 775 780
 Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
 785 790 795 800
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
 805 810 815
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
 820 825 830
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
 835 840 845
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
 850 855 860
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
 945 950 955

<210> 563
 <211> 1517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1494)
 <223> RXA01745

<400> 563
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 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
 130 135 140
 gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag 480
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160
 cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct 528
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175
 act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac 576
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190
 gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc 624

Val	Pro	Tyr	Val	Thr	Pro	Leu	Val	Arg	Lys	Leu	Ala	Glu	Lys	His	Gly		
		195					200					205					
gtt	gac	ttg	aac	acc	gtg	acc	ggg	acc	ggg	atc	ggg	ggc	cgt	atc	cgc	672	
Val	Asp	Leu	Asn	Thr	Val	Thr	Gly	Thr	Gly	Ile	Gly	Gly	Arg	Ile	Arg		
	210					215					220						
aag	cag	gat	gtt	ttg	gct	gct	gcg	aac	ggc	gag	gct	gca	cct	gct	gag	720	
Lys	Gln	Asp	Val	Leu	Ala	Ala	Ala	Asn	Gly	Glu	Ala	Ala	Pro	Ala	Glu		
	225				230					235					240		
gct	gct	gct	cct	gtt	tcc	gct	tgg	tcc	act	aag	tct	gtt	gac	cct	gag	768	
Ala	Ala	Ala	Pro	Val	Ser	Ala	Trp	Ser	Thr	Lys	Ser	Val	Asp	Pro	Glu		
				245				250						255			
aag	gct	aag	ctc	cgt	ggg	acc	act	cag	aag	gtc	aac	cgc	atc	cgt	gag	816	
Lys	Ala	Lys	Leu	Arg	Gly	Thr	Thr	Gln	Lys	Val	Asn	Arg	Ile	Arg	Glu		
			260					265					270				
atc	acc	gcg	atg	aag	acc	gtc	gag	gct	ctg	cag	att	tct	gct	cag	ctc	864	
Ile	Thr	Ala	Met	Lys	Thr	Val	Glu	Ala	Leu	Gln	Ile	Ser	Ala	Gln	Leu		
		275					280					285					
acc	cag	ctg	cac	gag	gtc	gat	atg	act	cgc	gtt	gct	gag	ctg	cgt	aag	912	
Thr	Gln	Leu	His	Glu	Val	Asp	Met	Thr	Arg	Val	Ala	Glu	Leu	Arg	Lys		
	290					295					300						
aag	aac	aag	ccc	gcg	ttc	atc	gag	aag	cac	ggg	gtg	aac	ctc	act	tac	960	
Lys	Asn	Lys	Pro	Ala	Phe	Ile	Glu	Lys	His	Gly	Val	Asn	Leu	Thr	Tyr		
	305				310					315					320		
ctg	cca	ttc	ttc	gtg	aag	gca	gtt	gtc	gag	gct	ttg	gtt	tcc	cat	cca	1008	
Leu	Pro	Phe	Phe	Val	Lys	Ala	Val	Val	Glu	Ala	Leu	Val	Ser	His	Pro		
				325					330					335			
aac	gtc	aac	gcg	tct	ttc	aac	gcg	aag	acc	aag	gag	atg	acc	tac	cac	1056	
Asn	Val	Asn	Ala	Ser	Phe	Asn	Ala	Lys	Thr	Lys	Glu	Met	Thr	Tyr	His		
			340					345					350				
tcc	tcc	gtt	aac	ctc	tcc	atc	gct	gtt	gat	acc	cca	gct	ggg	ctg	ttg	1104	
Ser	Ser	Val	Asn	Leu	Ser	Ile	Ala	Val	Asp	Thr	Pro	Ala	Gly	Leu	Leu		
		355					360					365					
acc	cca	gtc	att	cac	gat	gct	cag	gat	ctc	tcc	atc	cca	gag	atc	gca	1152	
Thr	Pro	Val	Ile	His	Asp	Ala	Gln	Asp	Leu	Ser	Ile	Pro	Glu	Ile	Ala		
	370					375					380						
aag	gca	att	gtt	gac	ctg	gct	gat	cgt	tca	cgc	aac	aac	aag	ctg	aag	1200	
Lys	Ala	Ile	Val	Asp	Leu	Ala	Asp	Arg	Ser	Arg	Asn	Asn	Lys	Leu	Lys		
	385				390					395					400		
cca	aac	gat	ctg	tcc	ggg	ggc	acc	ttc	acc	atc	acc	aac	att	ggg	tct	1248	
Pro	Asn	Asp	Leu	Ser	Gly	Gly	Thr	Phe	Thr	Ile	Thr	Asn	Ile	Gly	Ser		
				405					410					415			
gaa	ggc	gca	ctg	tct	gat	acc	cca	atc	ctg	gtt	cca	cca	cag	gct	ggc	1296	
Glu	Gly	Ala	Leu	Ser	Asp	Thr	Pro	Ile	Leu	Val	Pro	Pro	Gln	Ala	Gly		
			420					425					430				
atc	ttg	ggc	acc	ggc	gcg	atc	gtg	aag	cgt	cca	gtt	gtc	atc	acc	gag	1344	
Ile	Leu	Gly	Thr	Gly	Ala	Ile	Val	Lys	Arg	Pro	Val	Val	Ile	Thr	Glu		

435	440	445	
gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg			1392
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu			
450	455	460	
acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg			1440
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu			
465	470	475	480
acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg			1488
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu			
485	490	495	
cag ctc taagatctct gcaagttaaa acc			1517
Gln Leu			

<210> 564

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly	Ala	Val	Ile	Ala
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Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Ala
			20					25					30		

Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu	Pro	Lys	Lys	Glu
		35					40					45			

Ala	Ala	Pro	Glu	Ala	Pro	Ala	Ala	Thr	Gly	Ala	Ala	Thr	Asp	Val	Glu
	50					55					60				

Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	Thr	Ile	Thr	Gln	Trp
65					70					75					80

Leu	Lys	Ala	Val	Gly	Asp	Thr	Val	Glu	Val	Asp	Glu	Pro	Leu	Leu	Glu
			85						90					95	

Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	Ser	Pro	Val	Ala	Gly
			100					105					110		

Thr	Ile	Val	Glu	Ile	Leu	Ala	Asp	Glu	Asp	Asp	Thr	Val	Asp	Val	Gly
		115					120					125			

Ala	Val	Ile	Ala	Arg	Ile	Gly	Asp	Ala	Asn	Ala	Ala	Ala	Ala	Pro	Ala
	130					135					140				

Glu	Glu	Glu	Ala	Ala	Pro	Ala	Glu	Glu	Glu	Glu	Pro	Val	Lys	Glu	Glu
145					150					155				160	

Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Glu	Pro	Lys	Lys	Glu	Ala	Ala
			165						170					175	

Thr	Thr	Pro	Ala	Ala	Ala	Ser	Ala	Thr	Val	Ser	Ala	Ser	Gly	Asp	Asn
			180					185						190	

Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
 195 200 205
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
 210 215 220
 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
 225 230 235 240
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
 245 250 255
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
 260 265 270
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
 275 280 285
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
 290 295 300
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
 305 310 315 320
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
 325 330 335
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
 340 345 350
 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
 355 360 365
 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
 370 375 380
 Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
 385 390 395 400
 Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
 405 410 415
 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
 420 425 430
 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
 435 440 445
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
 450 455 460
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
 465 470 475 480
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
 485 490 495
 Gln Leu

atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att 643
Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile
170 175 180

ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc 691
 Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala
 185 190 195
 ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc 739
 Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile
 200 205 210
 ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg 787
 Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val
 215 220 225
 aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga 835
 Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly
 230 235 240 245
 aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act 883
 Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr
 250 255 260
 gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga 931
 Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly
 265 270 275
 aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct 979
 Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala
 280 285 290
 ttg taactaacag gccacagatc tta 1005
 Leu

<210> 566

<211> 294

<212> PRT

<213> Corynebacterium glutamicum

<400> 566

Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile
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 20 25 30
 Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile
 35 40 45
 Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala
 50 55 60
 Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala
 65 70 75 80
 Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu
 85 90 95
 Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala
 100 105 110
 Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn

115	120	125	
Cys Pro Gly Ile Ile Thr	Pro Gly Glu Ser Leu	Ala Gly Ile Thr Pro	
130	135	140	
Ala Asn Ile Ala Gly Ser Gly	Pro Ile Gly Leu Ile Ser Lys Ser Gly		
145	150	155	160
Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser			
	165	170	175
Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile			
	180	185	190
Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val			
	195	200	205
Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe			
	210	215	220
Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe			
	225	230	235
Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr			
	245	250	255
Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val			
	260	265	270
Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg			
	275	280	285
Glu Val Val Ala Ala Leu			
	290		
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<223> RXA00783			
<400> 567			
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tttacagtgt tagacttcac aatacgatca tattggtgag ttg aaa cac tta ctt 115			
Leu Lys His Leu Leu 5			
1			
tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163			
Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro 20			
10 15			
gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211			
Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu 35			
25 30			

ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca	259
Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr	
40 45 50	
cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc	307
Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val	
55 60 65	
gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc	355
Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val	
70 75 80 85	
cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att	403
Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile	
90 95 100	
ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg	451
Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala	
105 110 115	
cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat	499
Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp	
120 125 130	
cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg	547
Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met	
135 140 145	
gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg	595
Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val	
150 155 160 165	
gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att	643
Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile	
170 175 180	
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg	691
Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro	
185 190 195	
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc	739
Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu	
200 205 210	
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg	787
Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala	
215 220 225	
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat	835
Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp	
230 235 240 245	
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa	883
Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu	
250 255 260	
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct	931
Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser	
265 270 275	
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat	979

Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp
 280 285 290

atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac 1027
 Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn
 295 300 305

ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt 1075
 Phe Leu Asp Ile Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly
 310 315 320 325

ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat 1123
 Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn
 330 335 340

gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt 1171
 Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val
 345 350 355

gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg 1219
 Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val
 360 365 370

cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa 1267
 Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu
 375 380 385

tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct 1315
 Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala
 390 395 400 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala
 410 415 420

acc gct aat tagttaagga gcacctgttt aat 1395
 Thr Ala Asn

<210> 568

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

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Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr
 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly
 35 40 45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile
 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly
 65 70 75 80

Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp
 85 90 95
 Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn
 100 105 110
 Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe
 115 120 125
 Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser
 130 135 140
 Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu
 145 150 155 160
 Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp
 165 170 175
 Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala
 180 185 190
 Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu
 195 200 205
 Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp
 210 215 220
 Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala
 225 230 235 240
 Asp Phe Arg His Asp Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly
 245 250 255
 Leu Asp Ile Leu Glu Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val
 260 265 270
 Lys Leu Asp Gly Ser Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val
 275 280 285
 Met Ser Thr Leu Asp Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly
 290 295 300
 Gln Arg Pro Ala Asn Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu
 305 310 315 320
 Ser Met Ala Ala Gly Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg
 325 330 335
 Ser Val Phe Val Asn Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val
 340 345 350
 Ala Lys Gly Ile Val Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr
 355 360 365
 Lys Pro Leu Val Val Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg
 370 375 380
 Arg Ile Leu Ala Glu Tyr Asn His Pro Leu Val Thr Val Val Glu Gly
 385 390 395 400
 Met Asp Ala Ala Ala Asp His Ala Ala His Leu Ala Asn Leu Ala Gln

405

410

415

His Gly Gln Phe Ala Thr Ala Asn
420

<210> 569

<211> 1623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1600)

<223> RXN01695

<400> 569

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tggtcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg 115
Met Ser Asp Ser Pro
1 5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
10 15 20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu
25 30 35

cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa 259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln
40 45 50

gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta 307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu
55 60 65

tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc 355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala
70 75 80 85

aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg 403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp
90 95 100

tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc 451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile
105 110 115

aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca 499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala
120 125 130

tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag 547
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln
135 140 145

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595
Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro

150	155	160	165	
ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg				643
Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp				
	170	175	180	
atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac				691
Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr				
	185	190	195	
ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa				739
Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu				
	200	205	210	
gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag				787
Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys				
	215	220	225	
aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc				835
Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe				
	230	235	240	245
gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc				883
Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile				
	250	255	260	
cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt				931
Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu				
	265	270	275	
cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat				979
Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr				
	280	285	290	
ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac				1027
Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp				
	295	300	305	
acc cgc gtt atc gag ggt gaa aag ggt ctg ctc ttt gga cct tac ggt				1075
Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu Phe Gly Pro Tyr Gly				
	310	315	320	325
ggc tgg acc cct aag ttc ttg aag gaa ggc tcc tac ctg gac ctg ttc				1123
Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser Tyr Leu Asp Leu Phe				
	330	335	340	
aag tcc atc cgc cca gac aac att cct tcc tac ctt ggc gtt gct gct				1171
Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr Leu Gly Val Ala Ala				
	345	350	355	
cag gaa ttt gat ctg acc aag tac ctt gtc act gaa gtt ctc aag gac				1219
Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr Glu Val Leu Lys Asp				
	360	365	370	
cag gac aag cgt atg gat gct ctt cgc gag tac atg cca gag gca caa				1267
Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr Met Pro Glu Ala Gln				
	375	380	385	
aac ggc gat tgg gag acc atc gtt gcc gga cag cgt gtt cag gtt att				1315
Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln Arg Val Gln Val Ile				
	390	395	400	405

aag cct gca gga ttc cct aag ttc ggt tcc ctg gaa ttc ggc acc acc 1363
 Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu Glu Phe Gly Thr Thr
 410 415 420

 ttg atc aac aac tcc gaa ggc acc atc gcc gga ttg ctc ggt gct tcc 1411
 Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly Leu Leu Gly Ala Ser
 425 430 435

 cct gga gca tcc atc gca cct tcc gca atg atc gag ctg ctt gag cgt 1459
 Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile Glu Leu Leu Glu Arg
 440 445 450

 tgc ttc ggt gac cgc atg atc gag tgg ggc gac aag ctg aag gac atg 1507
 Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp Lys Leu Lys Asp Met
 455 460 465

 atc cct tcc tac ggc aag aag ctt gct tcc gag cca gca ctg ttt gag 1555
 Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu Pro Ala Leu Phe Glu
 470 475 480 485

 cag cag tgg gca cgc acc cag aag acc ctg aag ctt gag gaa gcc 1600
 Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys Leu Glu Glu Ala
 490 495 500

 taaatcttct aactgctttc ttt 1623

<210> 570

<211> 500

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 570

Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
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 20 25 30

 Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
 35 40 45

 Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50 55 60

 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65 70 75 80

 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
 85 90 95

 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
 100 105 110

 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115 120 125

 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130 135 140

His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
 290 295 300
 Val Pro His Leu Asp Thr Arg Val Ile Glu Gly Glu Lys Gly Leu Leu
 305 310 315 320
 Phe Gly Pro Tyr Gly Gly Trp Thr Pro Lys Phe Leu Lys Glu Gly Ser
 325 330 335
 Tyr Leu Asp Leu Phe Lys Ser Ile Arg Pro Asp Asn Ile Pro Ser Tyr
 340 345 350
 Leu Gly Val Ala Ala Gln Glu Phe Asp Leu Thr Lys Tyr Leu Val Thr
 355 360 365
 Glu Val Leu Lys Asp Gln Asp Lys Arg Met Asp Ala Leu Arg Glu Tyr
 370 375 380
 Met Pro Glu Ala Gln Asn Gly Asp Trp Glu Thr Ile Val Ala Gly Gln
 385 390 395 400
 Arg Val Gln Val Ile Lys Pro Ala Gly Phe Pro Lys Phe Gly Ser Leu
 405 410 415
 Glu Phe Gly Thr Thr Leu Ile Asn Asn Ser Glu Gly Thr Ile Ala Gly
 420 425 430
 Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala Met Ile
 435 440 445
 Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp Gly Asp
 450 455 460
 Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala Ser Glu

465	470	475	480
Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr Leu Lys			
	485	490	495
Leu Glu Glu Ala			
500			
<210> 571			
<211> 1039			
<212> DNA			
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<222> (101)..(1039)			
<223> FRXA01615			
<400> 571			
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tgttcggcag agaactcgcg	gagataaaag gaagttgaac	atg tca gat tcc ccg	115
		Met Ser Asp Ser Pro	
		1 5	
aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt			163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly			
	10	15	20
gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag			211
Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met Leu Arg Gln Leu Glu			
	25	30	35
cca agc tgg act cag atc gtc ttc gag cgt ttg gat gga ccg gca caa			259
Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu Asp Gly Pro Ala Gln			
	40	45	50
gag tcg tcc tcc ccg tgg aac aat gca gga acc ggc cac tct gct cta			307
Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr Gly His Ser Ala Leu			
	55	60	65
tgc gag ctg aac tac acc cca gag gtt aag ggc aag gtt gaa att gcc			355
Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly Lys Val Glu Ile Ala			
	70	75	80
aag gct gta gga atc aac gag aag ttc cag gtt tcc cgt cag ttc tgg			403
Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val Ser Arg Gln Phe Trp			
	90	95	100
tct cac ctc gtt gaa gag gga gtg ctg tct gat cct aag gaa ttc atc			451
Ser His Leu Val Glu Glu Gly Val Leu Ser Asp Pro Lys Glu Phe Ile			
	105	110	115
aac cct gtt cct cac gta tct ttc ggc cag ggc gca gat cag gtt gca			499
Asn Pro Val Pro His Val Ser Phe Gly Gln Gly Ala Asp Gln Val Ala			
	120	125	130
tac atc aag gct cgc tac gaa gct ttg aag gat cac cca ctc ttc cag			547
Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp His Pro Leu Phe Gln			
	135	140	145

ggc atg acc tac gct gac gat gaa gct acc ttc acc gag aag ctg cct 595
 Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe Thr Glu Lys Leu Pro
 150 155 160 165

 ttg atg gca aag ggc cgt gac ttc tct gat cca gta gca atc tct tgg 643
 Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro Val Ala Ile Ser Trp
 170 175 180

 atc gat gaa ggc acc gac atc aac tac ggt gct cag acc aag cag tac 691
 Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala Gln Thr Lys Gln Tyr
 185 190 195

 ctg gat gca gct gaa gtt gaa ggc act gaa atc cgc tat ggc cac gaa 739
 Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile Arg Tyr Gly His Glu
 200 205 210

 gtc aag agc atc aag gct gat ggc gca aag tgg atc gtg acc gtc aag 787
 Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp Ile Val Thr Val Lys
 215 220 225

 aac gta cac act ggc gac acc aag acc atc aag gca aac ttc gtg ttc 835
 Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys Ala Asn Phe Val Phe
 230 235 240 245

 gtc ggc gca ggc gga tac gca ctg gat ctg ctt cgc agc gca ggc atc 883
 Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu Arg Ser Ala Gly Ile
 250 255 260

 cca cag gtc aag ggc ttc gct gga ttc cca gta tcc ggc ctg tgg ctt 931
 Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val Ser Gly Leu Trp Leu
 265 270 275

 cgt tgc acc aac gag gaa ctg atc gag cag cac gca gcc aag gta tat 979
 Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His Ala Ala Lys Val Tyr
 280 285 290

 ggc aag gca tct gtt ggc gct cct cca atg tct gtt cct cac ctt gac 1027
 Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser Val Pro His Leu Asp
 295 300 305

 acc cgc gtt atc 1039
 Thr Arg Val Ile
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<210> 572

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

Met Ser Asp Ser Pro Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp
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Val Val Leu Ile Gly Ala Gly Ile Met Ser Ser Thr Leu Gly Ala Met
 20 25 30

Leu Arg Gln Leu Glu Pro Ser Trp Thr Gln Ile Val Phe Glu Arg Leu
 35 40 45

Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50 55 60
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65 70 75 80
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
 85 90 95
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
 100 105 110
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115 120 125
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130 135 140
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
 275 280 285
 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser
 290 295 300
 Val Pro His Leu Asp Thr Arg Val Ile
 305 310

<210> 573

<211> 233

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(210)

<223> FRXA01695

<400> 573

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Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
  1             5             10             15

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atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg 96
Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
      20             25             30

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ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct 144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
      35             40             45

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tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc 192
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
      50             55             60

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ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt 233
Leu Lys Leu Glu Glu Ala
  65             70

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<210> 574

<211> 70

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 574

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Ala Gly Leu Leu Gly Ala Ser Pro Gly Ala Ser Ile Ala Pro Ser Ala
  1             5             10             15

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Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp
      20             25             30

```

```

Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
      35             40             45

```

```

Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
      50             55             60

```

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Leu Lys Leu Glu Glu Ala
  65             70

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<210> 575

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1063)

<223> RXA00290

<400> 575

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agctacagat ttagctagtgt tttttgttcc agaaccctaa atgaggttct acccttaaca 60

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
Met Thr Ile Asp Leu
      1             5

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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

<210> 576

<211> 321

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 576

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

180	185	190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val		
195	200	205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser		
210	215	220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala		
225	230	235
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn		
245	250	255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn		
260	265	270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe		
275	280	285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys		
290	295	300
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg		
305	310	315
		320
Ser		

<210> 577
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXN01048

<400> 577
 agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60
 gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly

55	60	65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc			355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly			
70	75	80	85
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag			403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln			
	90	95	100
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac			451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp			
	105	110	115
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct			499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro			
	120	125	130
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc			547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe			
	135	140	145
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac			595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His			
	150	155	160
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac			643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn			
	170	175	180
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att			691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile			
	185	190	195
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac			739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn			
	200	205	210
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac			787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His			
	215	220	225
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag			835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys			
	230	235	240
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc			883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly			
	250	255	260
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct			931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala			
	265	270	275
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca			979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro			
	280	285	290
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc			1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val			
	295	300	305

gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg 1075
 Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala
 310 315 320 325

ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc 1123
 Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile
 330 335 340

acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag 1171
 Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln
 345 350 355

ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc 1219
 Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370

gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385

aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405

cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 578

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 578

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
 1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser

130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp 145 150 155 160		
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu 165 170 175		
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp 180 185 190		
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val 195 200 205		
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser 210 215 220		
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala 225 230 235 240		
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn 245 250 255		
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn 260 265 270		
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe 275 280 285		
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys 290 295 300		
Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile 305 310 315 320		
Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala 325 330 335		
Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln 340 345 350		
Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu 355 360 365		
Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg 370 375 380		
Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser 385 390 395 400		
Leu Pro Val Glu Ala Pro Ile Phe 405		

<210> 579

<211> 311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(288)

<223> FRXA01048

<400> 579

cgc tct gac ttg cct aac cag atc aac aac gtg ctg gcg ttc cca gga 48
 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45

tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95

taagagcaaa cttgaggccc aca 311

<210> 580

<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95

<210> 581

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1063)

<223> FRXA00290

<400> 581

agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
 55 60 65

aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70 75 80 85

gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
 90 95 100

ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
 105 110 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
 Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
 120 125 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
 Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
 135 140 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile

185	190	195	
tcc ggc gca ggc gca ggc ggc gtt gca gct gta gat atg ctg acc aac			739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn			
200	205	210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac			787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His			
215	220	225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag			835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys			
230	235	240	245
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc			883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly			
250	255	260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct			931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala			
265	270	275	
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca			979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro			
280	285	290	
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc			1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val			
295	300	305	
gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca			1063
Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser			
310	315	320	

<210> 582

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 582

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
1 5 10 15

Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 583
 <211> 582
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(582)
 <223> RXN03101

<400> 583
 atc ctt gca gac gaa gac gac acc gtc gac gtc ggc gca gtc atc gcc 48
 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
 1 5 10 15
 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala

	20	25	30	
gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag				144
Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu				
	35	40	45	
gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa				192
Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu				
	50	55	60	
atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg				240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp				
	65	70	75	80
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag				288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu				
	85	90	95	
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc				336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly				
	100	105	110	
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc				384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly				
	115	120	125	
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc				432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala				
	130	135	140	
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag				480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu				
	145	150	155	160
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct				528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala				
	165	170	175	
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac				576
Thr Thr Pro Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn				
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gtt cca				582
Val Pro				

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<212> PRT

<213> Corynebacterium glutamicum

<400> 584

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 20 25 30

Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45

Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60

Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80

Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95

Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110

Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125

Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala
 130 135 140

Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
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Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
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Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
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Val Pro

<210> 585
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 <213> Corynebacterium glutamicum

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 <222> (101)..(517)
 <223> RXN02046

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aaattattaa catccgacgc aacgcttcag gagagtcctc atg aaa gag aca ctg 115
 Met Lys Glu Thr Leu
 1 5

acc acc ggt tta acc cac caa atg acc tac ata gtg cca gca aac cgc 163
 Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile Val Pro Ala Asn Arg
 10 15 20

aca gtt ccg cat ctg ctt ccc gaa gca gca gaa ttt gaa acc atg cca 211
 Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu Phe Glu Thr Met Pro
 25 30 35

gat gtc ctg gcc act gga tat atg gtc ggc atc atc gag tgg gcc tgc 259
 Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile Ile Glu Trp Ala Cys
 40 45 50

atg gaa ctt ctg cgt ccc cat ttg gac gac ggt gaa atc tcg ctg ggc 307
 Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly Glu Ile Ser Leu Gly
 55 60 65
 act cat gtg aac ttc tcc cac gca gct cca acg gtt cct gga tcc acg 355
 Thr His Val Asn Phe Ser His Ala Ala Pro Thr Val Pro Gly Ser Thr
 70 75 80 85
 gtc acc atc gat gtt gag gtg aca gag atc aac cgt cgt gca gtt acc 403
 Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn Arg Arg Ala Val Thr
 90 95 100
 ttc aac atc act gca gct gat gag ttc gcc acc atc agc acc ggc acc 451
 Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr Ile Ser Thr Gly Thr
 105 110 115
 cac cag cgc ggt gtg gtt aac cgt gag aag ttt gtc tcc cgt ctg cct 499
 His Gln Arg Gly Val Val Asn Arg Glu Lys Phe Val Ser Arg Leu Pro
 120 125 130
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 Glu Ala Pro Lys Glu Asn
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<210> 586

<211> 139

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 586

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 20 25 30
 Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45
 Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60
 Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80
 Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
 85 90 95
 Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
 100 105 110
 Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe
 115 120 125
 Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
 130 135

<210> 587

<211> 1683

<212> DNA

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<220>

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<222> (101)..(1660)

<223> RXN00389

<400> 587

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                                     Met Ile Thr Ala Thr
                                     1 5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
                        10 15 20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
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cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
                        40 45 50

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Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu Thr Thr Pro Glu Val
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aga gca gat ttc ctg gat tcc atc gct gac aac atc gat gcg cta tcc 355
Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn Ile Asp Ala Leu Ser
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ggc gag atc gtg caa cgg gcg agc ctg gag aca ggt ttg gga act acc 403
Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr Gly Leu Gly Thr Thr
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cga ctc aca ggc gaa gta gcc cgc acc agc aac cag ctc cgc ctg ttt 451
Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn Gln Leu Arg Leu Phe
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gca gaa acc gtg aga agc gga cag ttc cac cga gta cgc att gaa cga 499
Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg Val Arg Ile Glu Arg
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gga ccg cgg att gat ctt cgc cag cgt cag gtt ccg ttg gga cca gtc 547
Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val Pro Leu Gly Pro Val
                        135 140 145

gcg gta ttc ggg gca agc aac ttc ccc gtc gct ttc tct act gct ggt 595
Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala Phe Ser Thr Ala Gly
                        150 155 160 165

ggc gat aca gca tca gcg ttg gct gca ggc tgc cct gtg gtt ttt aag 643
Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys Pro Val Val Phe Lys
                        170 175 180

gcg cat aat gcg cac cct gga aca gct gag ctc gtc ggg caa gcg gtg 691
Ala His Asn Ala His Pro Gly Thr Ala Glu Leu Val Gly Gln Ala Val

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185	190	195	
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gtc tac ggc cgt ggc gtg gaa att ggc cag gag ctg gct gcg gat ccg Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu Leu Ala Ala Asp Pro 215 220 225			787
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gaa atg agt gcc acc aac cct gtg ttc gtc ttc ccc ggc gcg ctg gcg Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe Pro Gly Ala Leu Ala 265 270 275			931
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acc ggc agt tcc ggg caa ttg tgc acc aag cct ggc ctc gtt ttc atc Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro Gly Leu Val Phe Ile 295 300 305			1027
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys 310 315 320 325			1075
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gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys 345 350 355			1171
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cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser 390 395 400 405			1315
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr 410 415 420			1363
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu 425 430 435			1411

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 Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp
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cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat 1507
 Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr
 455 460 465

ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc 1555
 Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile
 470 475 480 485

gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg 1603
 Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu
 490 495 500

ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa 1651
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ata gac cgt taatagctgg tctttacatt tgc 1683
 Ile Asp Arg
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<210> 588
 <211> 520
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 588
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Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
 35 40 45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
 50 55 60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65 70 75 80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
 85 90 95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
 100 105 110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
 115 120 125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
 130 135 140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
 145 150 155 160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
 165 170 175
 Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
 180 185 190
 Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
 195 200 205
 Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
 210 215 220
 Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
 225 230 235 240
 Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
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 Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
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 Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
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 Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
 290 295 300
 Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
 305 310 315 320
 Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
 325 330 335
 Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
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 Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
 355 360 365
 Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
 370 375 380
 Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
 385 390 395 400
 Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
 405 410 415
 Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
 420 425 430
 Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
 435 440 445
 Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
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 His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
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catcacgtcg	aaacagtgac	agtgcattag	ctcatacttt	gtg	gtc	ggc	acc	gcc								115			
				Val	Val	Gly	Thr	Ala								5			
				1															
cat tgc gaa tca gca ctt aag gaa gtg act ttg atg tca aac gtt gga																163			
His Cys Glu Ser Ala Leu Lys Glu Val Thr Leu Met Ser Asn Val Gly																			
	10											15						20	
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Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro																			
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Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser																			
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Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala																			
											105						110	115	
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Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn																			
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tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc																547			
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cgc gac caa cca ttc atc acc ggt gag cgc acc gca gaa ggc tac tac Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr 265 270 275			931
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 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
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aat 1467

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<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 590

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 35 40 45

Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
 50 55 60

Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
 65 70 75 80

Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 85 90 95

Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
 100 105 110

Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
 115 120 125

Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 130 135 140

Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
 145 150 155 160

Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 165 170 175

Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
 180 185 190

Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 195 200 205
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 210 215 220
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 225 230 235 240
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 245 250 255
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
 260 265 270
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
 275 280 285
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 290 295 300
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 305 310 315 320
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 325 330 335
 Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 340 345 350
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 355 360 365
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 370 375 380
 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 385 390 395 400
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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 <222> (101)..(1396)

<223> FRXA02399

<400> 591

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 Met Ser Asn Val Gly
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aag cca cgt acc gca cag gaa atc cag cag gat tgg gac acc aac cct 163
 Lys Pro Arg Thr Ala Gln Glu Ile Gln Gln Asp Trp Asp Thr Asn Pro
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cgt tgg aac ggc atc acc cgc gac tac acc gca gac cag gta gct gat 211
 Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
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ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
 Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
 40 45 50

gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
 Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
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gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
 Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
 70 75 80 85

ggc ctg aag gct gtc tac ctg tcc ggt tgg cag gtc gca ggt gac gcc 403
 Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln Val Ala Gly Asp Ala
 90 95 100

aac ctc tcc ggc cac acc tac cct gac cag tcc ctc tac cca gcg aac 451
 Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser Leu Tyr Pro Ala Asn
 105 110 115

tcc gtt cca agc gtc gtt cgt cgc atc aac aac gca ctg ctg cgt tcc 499
 Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn Ala Leu Leu Arg Ser
 120 125 130

gat gaa atc gca cgc acc gaa ggc gac acc tcc gtt gac aac tgg gtt 547
 Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser Val Asp Asn Trp Val
 135 140 145

gtc cca atc gtc gcg gac ggc gaa gct ggc ttc ggt gga gca ctc aac 595
 Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe Gly Gly Ala Leu Asn
 150 155 160 165

gtc tac gaa ctc cag aag gca atg atc gca gct ggc gct gca ggc acc 643
 Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala Gly Ala Ala Gly Thr
 170 175 180

cac tgg gaa gac cag ctc gct tct gaa aag aag tgt ggc cac ctc ggc 691
 His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys Cys Gly His Leu Gly
 185 190 195

ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct 739
 Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser
 200 205 210

gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca 787
 Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala
 215 220 225

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 Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu
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 Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr Ala Glu Gly Tyr Tyr
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cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac 931
 His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr
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gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg 979
 Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu
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 Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg Ser Glu Phe Pro Asp
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cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac 1075
 Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His
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 Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
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 Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala Arg Glu Gly Met Thr
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tcc ttc gtt gac ctg cag aac cgt gag ttc aag gca gct gaa gag cgt 1267
 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
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 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
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aat 1419

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Asp Gln Val Ala Asp Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu
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Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
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Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
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Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
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Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
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Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
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Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
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Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
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Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
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Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
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Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
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Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
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Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
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Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
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Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
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Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
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Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
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Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 340 345 350

Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
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Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
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Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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 Met Thr Glu Gln Glu
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 Val Thr Glu Ala Val Leu Pro Arg Val Gly Val Asp Ala Glu Lys Phe
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 Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg
 55 60 65

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Glu Leu Leu Ala Arg Arg Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr	
70 75 80 85	
cac cgc aac aac tcc ggc acc atc gac caa gag gcg tac gag gat ttc	403
His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe	
90 95 100	
ctc aaa gaa atc gga tac ttg gtt gag gag cca gaa gct gca gaa atc	451
Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro Glu Ala Ala Glu Ile	
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Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln	
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Leu Val Val Pro Ile Leu Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn	
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gct cgc tgg ggt tcc ctc tac gat gcg ttg tac ggc acc aac gcc atc	595
Ala Arg Trp Gly Ser Leu Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile	
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Pro Glu Thr Asp Gly Ala Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg	
170 175 180	
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Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe Leu Asp Ser Val Val	
185 190 195	
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Pro Leu Asp Gly Ala Ser His Ala Asp Val Glu Lys Tyr Asn Ile Thr	
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Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser Val Tyr Arg Leu Lys	
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Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile Glu Leu Gln Ile Asp	
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Val Leu Glu Ser Ala Ile Thr Thr Ile Met Asp Phe Glu Asp Ser Val	
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Ile	Phe	Thr	Arg	Glu	Leu	Asn	Lys	Asp	Arg	Val	Tyr	Ile	Gly	Arg	Asn	
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Gly	Thr	Glu	Leu	Val	Leu	His	Gly	Arg	Ser	Leu	Leu	Phe	Val	Arg	Asn	
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Pro	Gly	Ile	Ala	Pro	Gln	Asn	Lys	Met	Arg	Asn	Ser	Arg	Lys	Gly	Ser	
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atc	tac	atc	gtg	aag	cct	aag	cag	cac	ggc	cct	gaa	gaa	gtc	gcg	ttc	1363
Ile	Tyr	Ile	Val	Lys	Pro	Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	
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Thr	Asn	Glu	Leu	Phe	Gly	Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	
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His	Thr	Leu	Lys	Val	Gly	Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	
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Asn	Leu	Asp	Ala	Ser	Ile	Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	
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aac	act	ggc	ttc	ctg	gac	cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	1555
Asn	Thr	Gly	Phe	Leu	Asp	Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	
470				475					480					485		
gaa	gca	ggc	gcc	atg	gtg	cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	1603
Glu	Ala	Gly	Ala	Met	Val	Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	
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aag	cag	gcc	tac	gag	aac	aac	aac	gtt	gat	gca	ggt	att	cag	cgt	ggt	1651
Lys	Gln	Ala	Tyr	Glu	Asn	Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	
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ctt	cct	ggc	aag	gct	cag	atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	1699
Leu	Pro	Gly	Lys	Ala	Gln	Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	
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ctc	atg	gca	gaa	atg	ctg	gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	1747
Leu	Met	Ala	Glu	Met	Leu	Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	
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gcc	aac	act	gca	tgg	gtt	cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	1795
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Thr His Tyr His Leu Val Asp Val Phe Lys Val Gln Asp Glu Leu Arg				
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Ala Ala Gly Arg Arg Asp Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr				
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Ala Pro Asn Thr Asn Trp Ser Glu Glu Glu Lys Lys Glu Glu Met Asp				
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Gly Val Gly Cys Ser Lys Val Pro Asp Ile His Asp Ile Asp Leu Met				
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gaa gac cgc gca acg ctg cgt att tcc tcg cag atg ctg gcc aac tgg				2083
Glu Asp Arg Ala Thr Leu Arg Ile Ser Ser Gln Met Leu Ala Asn Trp				
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Ile Arg His Asp Val Val Ser Lys Glu Gln Val Leu Glu Ser Leu Glu				
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Arg Met Ala Val Val Val Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr				
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Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala				
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Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu				
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 Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly Thr Ile Asp Gln Glu
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 Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr Leu Val Glu Glu Pro
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 Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp Thr Glu Ile Ser Ser
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 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe
 180 185 190
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 Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala His Ile Gly Asp Ser
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 Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg Gly Phe Thr Gly Asn
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 Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr Asn Gly Leu His Ile
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 Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu Asn Lys Asp Arg Val
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 Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu His Gly Arg Ser Leu
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Ser Arg Lys Gly	Ser Ile Tyr Ile Val	Lys Pro Lys Gln His Gly Pro
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Glu Glu Val Ala Phe Thr	Asn Glu Leu Phe Gly Arg	Val Glu Asp Leu
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Ala Thr Leu His Ala Thr His Tyr His	Leu Val Asp Val Phe Lys Val	
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Arg Trp Val Glu His Gly Val Gly Cys	Ser Lys Val Pro Asp Ile His	
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Asp Ile Asp Leu Met Glu Asp Arg Ala Thr	Leu Arg Ile Ser Ser Gln	
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Met Leu Ala Asn Trp Ile Arg His Asp	Val Val Ser Lys Glu Gln Val	
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Leu Glu Ser Leu Glu Arg Met Ala Val	Val Val Asp Lys Gln Asn Ala	
675	680	685

Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys Tyr Asp Ala Ser Leu
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Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu Gly Thr Lys Ser Pro
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Ala Lys Asn

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Pro Arg Val Gly Val Asp Ala Glu Lys Phe Trp Ser Gly Phe Ala Ala
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Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
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gat gaa ctg cag atg ctt atc gac gac tac cac cgc aac aac tcc ggc 192
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
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acc atc gac caa gag gcg tac gag gat ttc ctc aaa gaa atc gga tac 240
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
65 70 75 80

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Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
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Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
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Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
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Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
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gat gct gtc ttg acc act gtt tgt gcc atc cca gga att gct ccg cag Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln 355 360 365	1104
aac aag atg cgc aat tcc cgc aag ggc tcc atc tac atc gtg aag cct Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro 370 375 380	1152
aag cag cac ggc cct gaa gaa gtc gcg ttc acc aac gag ctc ttc ggc	1200

Lys	Gln	His	Gly	Pro	Glu	Glu	Val	Ala	Phe	Thr	Asn	Glu	Leu	Phe	Gly		
385					390					395					400		
cgc	gtt	gag	gat	ctg	ctt	gat	ctg	cca	cgc	cac	acc	ttg	aag	gtt	ggt	1248	
Arg	Val	Glu	Asp	Leu	Leu	Asp	Leu	Pro	Arg	His	Thr	Leu	Lys	Val	Gly		
				405					410					415			
gtt	atg	gat	gag	gag	cgt	cgc	acg	tcc	gtg	aac	ctg	gat	gcc	agc	atc	1296	
Val	Met	Asp	Glu	Glu	Arg	Arg	Thr	Ser	Val	Asn	Leu	Asp	Ala	Ser	Ile		
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atg	gaa	gtt	gct	gac	cgc	ttg	gca	ttc	atc	aac	act	ggc	ttc	ctg	gac	1344	
Met	Glu	Val	Ala	Asp	Arg	Leu	Ala	Phe	Ile	Asn	Thr	Gly	Phe	Leu	Asp		
				435			440					445					
cgc	acc	ggc	gat	gaa	atc	cac	acc	tcc	atg	gaa	gca	ggc	gcc	atg	gtg	1392	
Arg	Thr	Gly	Asp	Glu	Ile	His	Thr	Ser	Met	Glu	Ala	Gly	Ala	Met	Val		
				450			455					460					
cgc	aag	gct	gat	atg	cag	acc	gca	ccg	tgg	aag	cag	gcc	tac	gag	aac	1440	
Arg	Lys	Ala	Asp	Met	Gln	Thr	Ala	Pro	Trp	Lys	Gln	Ala	Tyr	Glu	Asn		
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Asn	Asn	Val	Asp	Ala	Gly	Ile	Gln	Arg	Gly	Leu	Pro	Gly	Lys	Ala	Gln		
				485					490					495			
atc	ggt	aag	ggc	atg	tgg	gcg	atg	act	gaa	ctc	atg	gca	gaa	atg	ctg	1536	
Ile	Gly	Lys	Gly	Met	Trp	Ala	Met	Thr	Glu	Leu	Met	Ala	Glu	Met	Leu		
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gag	aag	aag	atc	ggc	cag	cca	cgc	gaa	ggc	gcc	aac	act	gca	tgg	gtt	1584	
Glu	Lys	Lys	Ile	Gly	Gln	Pro	Arg	Glu	Gly	Ala	Asn	Thr	Ala	Trp	Val		
				515			520					525					
cct	tca	cca	act	ggt	gcg	acg	ctg	cac	gca	acg	cac	tac	cac	ttg	gtt	1632	
Pro	Ser	Pro	Thr	Gly	Ala	Thr	Leu	His	Ala	Thr	His	Tyr	His	Leu	Val		
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gat	gtg	ttc	aag	gtt	caa	gac	gaa	ctg	cgt	gct	gcc	ggc	cgc	cgc	gac	1680	
Asp	Val	Phe	Lys	Val	Gln	Asp	Glu	Leu	Arg	Ala	Ala	Gly	Arg	Arg	Asp		
					550					555					560		
agc	ctg	cgc	aac	att	ctc	acc	att	tca	acc	gca	cca	aac	acc	aat	tgg	1728	
Ser	Leu	Arg	Asn	Ile	Leu	Thr	Ile	Ser	Thr	Ala	Pro	Asn	Thr	Asn	Trp		
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tct	gag	gaa	gag	aag	aag	gaa	gag	atg	gac	aac	aac	tgc	cag	tcc	atc	1776	
Ser	Glu	Glu	Glu	Lys	Lys	Glu	Glu	Met	Asp	Asn	Asn	Cys	Gln	Ser	Ile		
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ctc	gga	tac	gtt	gtg	cgc	tgg	gtt	gag	cac	ggt	gtt	ggt	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
				595			600					605					
gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cgc	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
				610			615					620					
cgt	att	tcc	tcg	cag	atg	ctg	gcc	aac	tgg	atc	cgc	cat	gat	gtt	gtc	1920	
Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val		

625	630	635	640	
tcg aag gag cag gtc ttg gag tca ctg gaa cga atg gca gtg gtc gtc				1968
Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val	645	650	655	
gac aag caa aat gcg ggc gac gag gcc tac cgc gat atg gcg ccg aag				2016
Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys	660	665	670	
tac gac gcc tcc ctc gcc ttc cag gcg gct aag gac ttg att ttc gaa				2064
Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu	675	680	685	
ggc acc aag tcc cca tcg ggc tac acc gag ccc atc ttg cac gca cgc				2112
Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg	690	695	700	
cgc cgc gag ttc aaa gca aaa aac taagcacgct ttccgacgct tac				2159
Arg Arg Glu Phe Lys Ala Lys Asn	705	710		

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<213> Corynebacterium glutamicum

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Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg	35	40	45	
Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly	50	55	60	
Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr	65	70	75	80
Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp	85	90	95	
Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu	100	105	110	
Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu	115	120	125	
Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala	130	135	140	
Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu	145	150	155	160
Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser	165	170	175	

His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
 180 185 190
 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
 195 200 205
 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
 210 215 220
 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
 225 230 235 240
 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
 245 250 255
 Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
 260 265 270
 Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
 275 280 285
 Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
 290 295 300
 Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
 305 310 315 320
 His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
 325 330 335
 Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
 340 345 350
 Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
 355 360 365
 Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
 370 375 380
 Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
 385 390 395 400
 Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
 405 410 415
 Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
 420 425 430
 Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
 435 440 445
 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
 450 455 460
 Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
 465 470 475 480
 Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
 485 490 495

Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
 500 505 510
 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
 515 520 525
 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
 530 535 540
 Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
 545 550 555 560
 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
 565 570 575
 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
 580 585 590
 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
 595 600 605
 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
 610 615 620
 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
 625 630 635 640
 Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val
 645 650 655
 Asp Lys Gln Asn Ala Gly Asp Glu Ala Tyr Arg Asp Met Ala Pro Lys
 660 665 670
 Tyr Asp Ala Ser Leu Ala Phe Gln Ala Ala Lys Asp Leu Ile Phe Glu
 675 680 685
 Gly Thr Lys Ser Pro Ser Gly Tyr Thr Glu Pro Ile Leu His Ala Arg
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 Arg Arg Glu Phe Lys Ala Lys Asn
 705 710

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 Leu Ser Arg Phe Ala
 1 5
 gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163

Ala	Asn	Leu	Ser	Leu	Thr	Phe	Thr	Glu	Leu	Asp	Phe	Leu	Asp	Arg	Phe		
				10					15					20			
gat	gcc	gct	tcg	aag	cat	gct	ttc	agt	gcc	gtg	gag	ttt	cag	tac	cct	211	
Asp	Ala	Ala	Ser	Lys	His	Ala	Phe	Ser	Ala	Val	Glu	Phe	Gln	Tyr	Pro		
			25					30					35				
tac	gat	ttc	gat	gtt	caa	gag	att	aaa	cag	cgt	gct	gat	tcc	gca	ggc	259	
Tyr	Asp	Phe	Asp	Val	Gln	Glu	Ile	Lys	Gln	Arg	Ala	Asp	Ser	Ala	Gly		
			40				45					50					
ctg	ccc	att	gaa	ctg	ttc	aat	gcc	cca	cct	ggg	gat	act	ttt	ggc	ctt	307	
Leu	Pro	Ile	Glu	Leu	Phe	Asn	Ala	Pro	Pro	Gly	Asp	Thr	Phe	Gly	Leu		
	55					60					65						
gcg	gca	ctg	gct	tcc	cct	gaa	gac	ttt	caa	caa	tcc	atc	gag	cag	gcc	355	
Ala	Ala	Leu	Ala	Ser	Pro	Glu	Asp	Phe	Gln	Gln	Ser	Ile	Glu	Gln	Ala		
	70				75				80						85		
atc	acg	tac	gcc	aca	gtg	ttg	aag	cca	aag	aag	atg	cat	gtc	atg	gct	403	
Ile	Thr	Tyr	Ala	Thr	Val	Leu	Lys	Pro	Lys	Lys	Met	His	Val	Met	Ala		
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Gly	Ile	Ala	Asp	Val	Thr	Ser	Glu	Thr	Thr	Ala	Arg	Tyr	Val	Glu	Asn		
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Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu	Asp	Val	Val	Val	Val		
		120					125					130					
att	gaa	cca	att	aat	cac	tat	tcg	gtt	ccc	ggc	tat	ttc	ctg	cac	act	547	
Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly	Tyr	Phe	Leu	His	Thr		
	135					140					145						
tta	gag	cag	gcg	tat	tgg	ctt	atc	gac	agc	att	gcc	cac	ccc	aat	gtg	595	
Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile	Ala	His	Pro	Asn	Val		
	150				155					160					165		
aag	atc	tta	ttc	gat	act	ttc	cac	ctt	cag	cag	att	cat	ggc	aat	ctc	643	
Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln	Ile	His	Gly	Asn	Leu		
				170					175					180			
acc	cgc	cgc	ctg	cgc	gag	gtt	cat	ggc	gca	ggc	ctt	ttg	gga	cac	gtg	691	
Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly	Leu	Leu	Gly	His	Val		
			185					190					195				
caa	gtg	gcc	tca	gtt	cct	gat	cga	cac	gaa	cct	ggc	act	ggc	gaa	gtc	739	
Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro	Gly	Thr	Gly	Glu	Val		
		200					205					210					
aat	gcg	gcg	tat	atc	ttc	caa	ctc	cta	agc	gaa	ctg	gga	tat	gac	ggc	787	
Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu	Leu	Gly	Tyr	Asp	Gly		
	215					220					225						
gtc	atc	gct	ggc	gaa	tac	cac	cct	gct	ggc	gaa	act	aca	gcc	ggc	ttg	835	
Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu	Thr	Thr	Ala	Gly	Leu		
	230				235				240						245		
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Gly	Trp	Leu	Glu	Leu													

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 35 40 45
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 50 55 60
 Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
 65 70 75 80
 Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
 85 90 95
 Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala
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 Arg Tyr Val Glu Asn Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu
 115 120 125
 Asp Val Val Val Val Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly
 130 135 140
 Tyr Phe Leu His Thr Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile
 145 150 155 160
 Ala His Pro Asn Val Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln
 165 170 175
 Ile His Gly Asn Leu Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly
 180 185 190
 Leu Leu Gly His Val Gln Val Ala Ser Val Pro Asp Arg His Glu Pro
 195 200 205
 Gly Thr Gly Glu Val Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu
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 Met Thr Phe Lys Leu
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gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163
 Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg
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gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211
 Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp
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tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259
 Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser
 40 45 50

tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307
 Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg
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gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag 355
 Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys
 70 75 80 85

ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag 403
 Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln
 90 95 100

gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc 451
 Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu
 105 110 115

tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca 499
 Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala
 120 125 130

ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc 547
 Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro
 135 140 145

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 Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala
 150 155 160 165

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 Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln
 170 175 180

att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc 691
 Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe
 185 190 195

atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc 739
 Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly
 200 205 210

acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg 787
 Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met
 215 220 225

ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc 835
 Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser
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agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt 884
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 35 40 45

Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
 50 55 60

Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
 65 70 75 80

Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
 85 90 95

Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
 100 105 110

Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
 115 120 125

Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
 130 135 140

Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
 145 150 155 160

Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp
 165 170 175

Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg
 180 185 190

Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly
 195 200 205

Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys
 210 215 220

Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp
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 245 250 255

Thr Val

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 Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu
 10 15 20

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 Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala
 25 30 35

gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg 199
 Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val
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 Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met
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gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt 295
 Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly
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ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act 343
 Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr
 90 95 100

gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac 391
 Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr
 105 110 115

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Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln	
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gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat	487
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr	
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Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys	
150 155 160 165	
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Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly	
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Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln	
185 190 195	
gca ttg cac acc acc acg gcg acg agg cag tcc cgt aaa ggt gcg att	679
Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile	
200 205 210	
tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc	727
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile	
215 220 225	
gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc	775
Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly Ala Pro Ser Pro Ile	
230 235 240 245	
tgg gaa ggc gaa gac ggc gta atc gcg tgg ctg ctg tcc ggt ctt gat	823
Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Leu Asp	
250 255 260	
cac atc tac acc att cct ttg cct gca gaa ggt gaa gcc aaa cga gca	871
His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly Glu Ala Lys Arg Ala	
265 270 275	
atc ttg gat acc tac acc aag gaa cac tcg gcg gaa tac cag tca cag	919
Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln	
280 285 290	
gca ccg atc gac ttg gcg cgc agc atg ggg gag aag ctg gca gca cag	967
Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu Lys Leu Ala Ala Gln	
295 300 305	
ggc ttg gac ctg cgt gat gtg gac tcc atc gtt ttg cac acc tcc cac	1015
Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val Leu His Thr Ser His	
310 315 320 325	
cac act cac tac gtg atc ggc acc gga tct aat gat cca cag aag ttc	1063
His Thr His Tyr Val Ile Gly Thr Gly Ser Asn Asp Pro Gln Lys Phe	
330 335 340	
gat cca gat gca tcg cga gaa acc ctt gat cac tcc atc atg tac att	1111
Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile	
345 350 355	
ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat	1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr	

360	365	370	
gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag			1207
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys			
375	380	385	
att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt			1255
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val			
390	395	400	405
gat cct gca gaa aag gcc ttc gcc gca cgc gca gtg atc acc ttc aag			1303
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys			
410	415	420	
gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct			1351
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro			
425	430	435	
ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc			1399
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg			
440	445	450	
acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg			1447
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu			
455	460	465	
gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac			1495
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn			
470	475	480	485
att gaa ttg gat gcc gat att ttg gcc aag gct cct gtg att ccg gaa			1543
Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala Pro Val Ile Pro Glu			
490	495	500	
gga ctg ttc tgatggcggg tttgttttcc tct			1575
Gly Leu Phe			

<210> 602

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 602

Met Ile Thr His Glu Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro			
1	5	10	15
Tyr Lys Lys His Leu Ala His Lys Met Ala Arg Val Ala Ala Asp Pro			
20	25	30	
Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile			
35	40	45	
Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser			
50	55	60	
Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly			
65	70	75	80
Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala			

868

Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 420 425 430

Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 435 440 445

Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 450 455 460

Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 465 470 475 480

Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 485 490 495

Pro Val Ile Pro Glu Gly Leu Phe
 500

<210> 603
 <211> 975
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(975)
 <223> FRXA00406

<400> 603
 gac cca gtt gag gtt gct gcg gac act cag gaa atg atc atc acc cgc 48
 Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1 5 10 15

atc atc gac aat gca tcg gtg cag gca gct tcc gtg ttg cgt cga cca 96
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
 20 25 30

gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt 144
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
 35 40 45

cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg 192
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50 55 60

gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac 240
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65 70 75 80

acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg 288
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
 85 90 95

att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc 336
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
 100 105 110

cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga 384
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly

115	120	125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca			432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro			
130	135	140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc			480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr			
145	150	155	160
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg			528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg			
165	170		175
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg			576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala			
180	185		190
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc			624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly			
195	200		205
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg			672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala			
210	215		220
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca			720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala			
225	230		235
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac			768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His			
245	250		255
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg			816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met			
260	265		270
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc			864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser			
275	280		285
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga			912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly			
290	295		300
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt			960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu			
305	310		315
gat cac tcc atc atg			975
Asp His Ser Ile Met			
325			

<210> 604

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

Asp Pro Val Glu Val Ala Ala Asp Thr Gln Glu Met Ile Ile Thr Arg
 1 5 10 15
 Ile Ile Asp Asn Ala Ser Val Gln Ala Ala Ser Val Leu Arg Arg Pro
 20 25 30
 Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly
 35 40 45
 Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp
 50 55 60
 Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp
 65 70 75 80
 Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro
 85 90 95
 Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile
 100 105 110
 Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly
 115 120 125
 Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro
 130 135 140
 Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr
 145 150 155 160
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
 165 170 175
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
 180 185 190
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
 195 200 205
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
 210 215 220
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
 225 230 235 240
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
 245 250 255
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
 260 265 270
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
 275 280 285
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
 290 295 300
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
 305 310 315 320
 Asp His Ser Ile Met

325

<210> 605
 <211> 431
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(408)
 <223> FRXA00514

<400> 605
 cac gag cgt tcc tat gct cct gag cga gcc ctc cgc cga gag acc atc 48
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
 20 25 30
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac 240
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa 288
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat 336
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct 384
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 cct gtg att ccg gaa gga ctg ttc tga tggcggg tttgttttcc tct 431
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 606
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 606
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
 1 5 10 15
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg

20	25	30
Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala		
35	40	45
Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val		
50	55	60
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr		
65	70	75
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu		
	85	90
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp		
	100	105
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala		
	115	120
Pro Val Ile Pro Glu Gly Leu Phe		
	130	135
<210> 607		
<211> 718		
<212> DNA		
<213> Corynebacterium glutamicum		
<220>		
<221> CDS		
<222> (101)..(718)		
<223> RXA00512		
<400> 607		
tacaacgagt acaacgcttt cgaccagcaa gtattcacct attccgctga cagctacaag	60	
cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca	115	
	Met Ser Ser Ala Thr	5
	1	
acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg	163	
Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr		
	10	15
gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc	211	
Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly		
	25	30
tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt	259	
Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe		
	40	45
tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag	307	
Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu		
	55	60
ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc	355	
Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile		
	70	75
		80
		85

tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
 Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
 90 95 100

cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451
 Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
 105 110 115

acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499
 Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
 120 125 130

ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547
 Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
 135 140 145

atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595
 Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
 150 155 160 165

atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643
 Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
 170 175 180

gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691
 Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
 185 190 195

aac gcc tcc acc ttc acc gcc cgc gtg 718
 Asn Ala Ser Thr Phe Thr Ala Arg Val
 200 205

<210> 608

<211> 206

<212> PRT

<213> Corynebacterium glutamicum

<400> 608

Met Ser Ser Ala Thr Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val
 1 5 10 15

Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
 20 25 30

Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser
 35 40 45

Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala
 50 55 60

Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu
 65 70 75 80

Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His
 85 90 95

Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
 100 105 110

Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His

115	120	125
Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg		
130	135	140
Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala		
145	150	155
Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala		
165	170	175
Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr		
180	185	190
Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val		
195	200	205

<210> 609
 <211> 320
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(297)
 <223> RXA00518

<400> 609

gtc ctt ccg gta tta gct gcc cgc cac gac ggc gaa aag tgg gtt gcc	48
Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala	
1 5 10 15	
atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag	96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys	
20 25 30	
ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc	144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe	
35 40 45	
ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc	192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly	
50 55 60	
tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc	240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg	
65 70 75 80	
cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att	288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile	
85 90 95	
gaa aag cgc taaaagattt tcgcttttcg acg	320
Glu Lys Arg	

<210> 610
 <211> 99
 <212> PRT

<213> Corynebacterium glutamicum

<400> 610

Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
 1 5 10 15
 Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
 20 25 30
 Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
 35 40 45
 Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
 50 55 60
 Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
 65 70 75 80
 Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
 85 90 95
 Glu Lys Arg

<210> 611

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXA01077

<400> 611

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 aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115
 Met Thr Glu Ser Gln
 1 5
 gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163
 Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
 10 15 20
 gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211
 Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
 25 30 35
 gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259
 Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
 40 45 50
 ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307
 Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
 55 60 65
 aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355
 Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg
 70 75 80 85

tac ctc gac ttc atg gac gcc tac cta gca aag ggc gaa acc aac cac	403
Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys Gly Glu Thr Asn His	
90 95 100	
ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc	451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly	
105 110 115	
gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta	499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val	
120 125 130	
cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat	547
His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp	
135 140 145	
cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca	595
His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala	
150 155 160 165	
ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga	643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly	
170 175 180	
aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac	691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His	
185 190 195	
tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca	739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala	
200 205 210	
gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa	787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu	
215 220 225	
ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat	835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp	
230 235 240 245	
tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa	883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys	
250 255 260	
cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa	931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu	
265 270 275	
ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac	979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His	
280 285 290	
ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa	1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu	
295 300 305	
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg	1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu	
310 315 320 325	

ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa 1123
 Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu
 330 335 340

cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg 1171
 Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met
 345 350 355

aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct 1219
 Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro
 360 365 370

gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg 1267
 Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val
 375 380 385

ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta 1315
 Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu
 390 395 400 405

gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc 1363
 Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe
 410 415 420

acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc 1411
 Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu
 425 430 435

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser
 440 445 450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494
 Thr Thr Arg Ser
 455

<210> 612
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 612
 Met Thr Glu Ser Gln Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu
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Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu
 20 25 30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val
 35 40 45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr
 50 55 60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn
 65 70 75 80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys
 85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala
 100 105 110
 Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala
 115 120 125
 Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg
 130 135 140
 Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala
 145 150 155 160
 Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala
 165 170 175
 Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr
 180 185 190
 Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys
 195 200 205
 Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro
 210 215 220
 Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly
 225 230 235 240
 Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg
 245 250 255
 Thr Ile Ile Lys Lys His Asn Ala Glu Ile His Ser Gln Ser Ala Leu
 260 265 270
 Asp Ala Ala Gln Glu Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn
 275 280 285
 Ile Glu Lys Ile His Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile
 290 295 300
 Gly Gly Gly Glu Glu Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu
 305 310 315 320
 Ala Asp His Ser Leu Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly
 325 330 335
 Gln Leu Asn Pro Glu Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp
 340 345 350
 Val Gln Thr Leu Met Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe
 355 360 365
 Ser Asp Arg Phe Pro Asp His Met Pro Ala Asp Leu Glu Val Thr Leu
 370 375 380
 Asn Asp Gly Ser Val Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe
 385 390 395 400
 His Asp Asn Pro Leu Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala
 405 410 415
 Leu Val Thr Pro Phe Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr

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                420                425                430
Ile Ile His Glu Leu Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala
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Leu Ala Lys Val Ser Thr Thr Arg Ser
      450                455

<210> 613
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(900)
<223> RXN03144

<400> 613
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Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp
   1                5                10                15

aag gcg ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg      96
Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
      20                25                30

gat cgt gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc      144
Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
      35                40                45

gaa gac ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat      192
Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
      50                55                60

cat gtg cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag      240
His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
      65                70                75                80

act tac aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att      288
Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
      85                90                95

gat ctg gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg      336
Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
      100               105               110

gaa cac att gca gag att gtg ctg cgc acc agt cac cac acg cat tat      384
Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
      115               120               125

gtg att ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc      432
Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
      130               135               140

tcg cgt gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg      480
Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
      145               150               155               160

ctt caa gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt      528

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Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 tcc acc cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg 576
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 gag gat cct gaa tgg acg cgc cga tac cat tct gat gat cct gca aaa 624
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 aag gcc ttt ggt gcg aaa gca gtg atc aca atg gct gat ggc acc gtg 672
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 att gag gat gaa ttg gct gtc gcg gat gcc cac ccg ctg ggt gct cgg 720
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 ccg ttt gcg ccg gag aat tac att gaa aaa ttc cgc aca ctc gcg cag 768
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 ggg att gtc att gat tca gaa cag gaa cgc ttc ttg cat gcc gtg caa 816
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 agc ctg cct gac ctg gat gat ctt gat cag ctc aac atc gaa gtc gac 864
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt 910
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
 290 295 300
 ttcgaatggt gtt 923

<210> 614

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 614

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 Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met
 20 25 30
 Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
 35 40 45
 Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
 50 55 60
 His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
 65 70 75 80
 Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
 85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
 100 105 110
 Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
 115 120 125
 Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
 130 135 140
 Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
 145 150 155 160
 Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175
 Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190
 Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205
 Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220
 Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240
 Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255
 Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270
 Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
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<211> 511

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(511)

<223> FRXA02322

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 ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115
 Met Arg Ile His Asp
 1 5

gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu
 10 15 20

gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro
 25 30 35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val
 40 45 50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa 307
 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln
 55 60 65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser
 70 75 80 85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta 403
 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val
 90 95 100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His
 105 110 115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga 499
 Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg
 120 125 130

agc agc ggc agg 511
 Ser Ser Gly Arg
 135

<210> 616

<211> 137

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
 1 5 10 15

Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
 20 25 30

Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
 35 40 45

Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
 50 55 60

Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
 65 70 75 80

Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
 85 90 95

Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala
 100 105 110

Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val
 115 120 125

Ala Gln Ala Gln Arg Ser Ser Gly Arg
 130 135

<210> 617

<211> 603

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(603)

<223> RXA02329

<400> 617

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Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
  1              5              10              15

ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt      96
Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
      20              25              30

gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac      144
Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
      35              40              45

ggg gtc atc gcg tgg ctg tta tcg ggc aaa gat cat gtt tat cat gtg      192
Gly Val Ile Ala Trp Leu Ser Gly Lys Asp His Val Tyr His Val
      50              55              60

cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac      240
Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
      65              70              75              80

aca aag gaa cat tca gcg gaa tat caa tcg cag gca ccg att gat ctg      288
Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
      85              90              95

gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac      336
Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
      100             105             110

att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att      384
Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
      115             120             125

ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tcg cgt      432
Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
      130             135             140

gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa      480
Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
      145             150             155             160

gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc      528
Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
      165             170             175

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cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat 576
 Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
 180 185 190

cct gaa tgg acg cgc cga tac cat tct 603
 Pro Glu Trp Thr Arg Arg Tyr His Ser
 195 200

<210> 618

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
 1 5 10 15

Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
 20 25 30

Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp
 35 40 45

Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val
 50 55 60

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
 65 70 75 80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
 85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
 100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
 115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
 130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
 145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
 165 170 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
 180 185 190

Pro Glu Trp Thr Arg Arg Tyr His Ser
 195 200

<210> 619

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02332

<400> 619

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tttgaccagc acattttcac ctacagaaaa ggagaaaaca atg agt gac agc caa 115
                                         Met Ser Asp Ser Gln
                                         1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
                        10 15 20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
                        25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
                        40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
                        55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc 355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile
                        70 75 80 85

cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca 403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala
                        90 95 100

gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc 451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala
                        105 110 115

gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg 499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met
                        120 125 130

gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca 547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala
                        135 140 145

cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt 595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe
                        150 155 160 165

ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat 643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp
                        170 175 180

ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc 691
Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser
                        185 190 195

aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg 739

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Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser
200                               205                               210

gcg atc aca ggt gcg atc ggt gct ctc aaa ggc cca ctg cac gga ggt 787
Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly
215                               220                               225

gcc aat gag ttt gtc atg cac acc atg ctg gat atc gac gat ccc aac 835
Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn
230                               235                               240                               245

aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc 883
Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile
250                               255                               260

atg gga ttc ggg cac cgc gtg tac aaa aac ggc gac tcc agg gtc ccc 931
Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro
265                               270                               275

tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa 979
Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln
280                               285                               290

aaa tgg gtg cac atg tat gag tgc atg caa gaa gtc atg gag gct cgc 1027
Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg
295                               300                               305

act ggc att aaa ccc aac ctc gac ttc ccg gcc ggc cct gcc tat tac 1075
Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr
310                               315                               320                               325

atg ctg gga ttc ccc gtc gac ttc ttc aca cca ctg ttt gtg ctg gcc 1123
Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro Leu Phe Val Leu Ala
330                               335                               340

cga gtg tca ggg tgg acg gca cac atc gtg gag caa ttt gaa aac aat 1171
Arg Val Ser Gly Trp Thr Ala His Ile Val Glu Gln Phe Glu Asn Asn
345                               350                               355

gcg ctg atc cga cca ttg tct gcc tac aac gga gtg gaa gaa agg gag 1219
Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly Val Glu Glu Arg Glu
360                               365                               370

gtg gtg ccc att tcg gag aga acc taatcagtga ggctgatttc taa 1266
Val Val Pro Ile Ser Glu Arg Thr
375                               380

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<210> 620

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

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Met Ser Asp Ser Gln Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp
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Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr
20           25           30

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Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu

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35					40					45					
Val	Ile	Tyr	Leu	Leu	Trp	Phe	Gly	Glu	Leu	Pro	Thr	Thr	Glu	Gln	Leu
50						55					60				
Arg	Thr	Phe	Asn	Thr	Thr	Gly	Arg	Ser	Tyr	Arg	Ser	Leu	Asp	Ala	Gly
65					70					75					80
Leu	Ile	Ser	Leu	Ile	His	Ser	Leu	Pro	Asn	Thr	Cys	His	Pro	Met	Asp
				85					90					95	
Val	Leu	Arg	Thr	Ala	Val	Ser	Tyr	Met	Gly	Thr	Phe	Asp	Pro	Asp	Pro
			100					105					110		
Phe	Thr	Arg	Asp	Ala	Asp	His	Ile	Arg	Ser	Ile	Gly	His	Asn	Leu	Leu
		115					120					125			
Ala	Gln	Leu	Pro	Met	Val	Val	Ala	Met	Asp	Ile	Arg	Arg	Arg	Ser	Gly
130						135					140				
Glu	Glu	Ile	Ile	Ala	Pro	Asp	His	Asn	Lys	Gly	Ile	Ala	Ser	Asn	Phe
145					150					155					160
Leu	Ser	Met	Val	Phe	Gly	Asn	Asp	Asp	Gly	Ser	Val	Ala	Asn	Ser	Ala
				165					170					175	
Asp	Asp	Ile	Arg	Asp	Phe	Glu	Arg	Ser	Leu	Ile	Leu	Tyr	Ala	Glu	His
			180					185					190		
Ser	Phe	Asn	Ala	Ser	Thr	Phe	Ser	Ala	Arg	Val	Ile	Ser	Ser	Thr	Arg
		195					200					205			
Ser	Asp	Thr	Tyr	Ser	Ala	Ile	Thr	Gly	Ala	Ile	Gly	Ala	Leu	Lys	Gly
	210					215					220				
Pro	Leu	His	Gly	Gly	Ala	Asn	Glu	Phe	Val	Met	His	Thr	Met	Leu	Asp
225					230					235					240
Ile	Asp	Asp	Pro	Asn	Asn	Ala	Ala	Asp	Trp	Met	Gly	Lys	Ala	Leu	Asp
				245					250					255	
Arg	Lys	Glu	Arg	Ile	Met	Gly	Phe	Gly	His	Arg	Val	Tyr	Lys	Asn	Gly
			260					265					270		
Asp	Ser	Arg	Val	Pro	Ser	Met	Glu	Lys	Ser	Met	Arg	Ser	Leu	Ala	Ala
		275					280					285			
Arg	His	Arg	Gly	Gln	Lys	Trp	Val	His	Met	Tyr	Glu	Ser	Met	Gln	Glu
	290					295					300				
Val	Met	Glu	Ala	Arg	Thr	Gly	Ile	Lys	Pro	Asn	Leu	Asp	Phe	Pro	Ala
305					310					315					320
Gly	Pro	Ala	Tyr	Tyr	Met	Leu	Gly	Phe	Pro	Val	Asp	Phe	Phe	Thr	Pro
				325					330					335	
Leu	Phe	Val	Leu	Ala	Arg	Val	Ser	Gly	Trp	Thr	Ala	His	Ile	Val	Glu
			340					345					350		
Gln	Phe	Glu	Asn	Asn	Ala	Leu	Ile	Arg	Pro	Leu	Ser	Ala	Tyr	Asn	Gly
		355					360					365			

Val Glu Glu Arg Glu Val Val Pro Ile Ser Glu Arg Thr
 370 375 380

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 <211> 1038
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1015)
 <223> RXN02333

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 Met Asn Leu Phe Ser
 1 5
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu
 10 15 20
 gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att 211
 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile
 25 30 35
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 Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly Val Tyr Val Ser Gly
 40 45 50
 gcc gtc ata gct gct gac ctg gca cta ccc gat atc ggc ttg acg acg 307
 Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp Ile Gly Leu Thr Thr
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 ctg acc gaa gtc gcc cac cgc gcg cgg caa att gcg cgc gtc aca gac 355
 Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile Ala Arg Val Thr Asp
 70 75 80 85
 cta gga gtg ctt gtc gac gcc gac acc ggc ttt ggc gaa ccc atg tcg 403
 Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe Gly Glu Pro Met Ser
 90 95 100
 gcc gca cgc acc gtc gcc gaa ttg gag gac gcc ggt gtg gcc gga tgc 451
 Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala Gly Val Ala Gly Cys
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 cac ctt gaa gac caa gtc aac ccc aaa cgt tgc ggg cac ttg gac ggc 499
 His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys Gly His Leu Asp Gly
 120 125 130
 aaa gaa gtc gtg cgc aca gac gtg atg gtt cga cgc atc gca gcc gcc 547
 Lys Glu Val Val Arg Thr Asp Val Met Val Arg Arg Ile Ala Ala Ala
 135 140 145
 gtc tcg gcc cgg cgc gac ccg aac ttt gtc atc tgc gcc cgc acc gac 595
 Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile Cys Ala Arg Thr Asp
 150 155 160 165

gcc gct gga gtg gaa gga atc gac gcc gcc att gag cgc gcg aaa gcc 643
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 tac tta gat gcg ggc gcc gac atg att ttc acc gaa gcc ctc cac agc 691
 Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr Glu Ala Leu His Ser
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 gaa gcc gac ttc cga tac ttc cgg cac gcc atc cct gat gcc ttg ttg 739
 Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile Pro Asp Ala Leu Leu
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 ctg gcg aat atg acc gaa ttt ggc aaa acg acg ctg ctg tca gcc gac 787
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 215 220 225
 gtg ttg gaa gag att ggc tac aac gcc gtg atc tac ccc gtg acc acg 835
 Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile Tyr Pro Val Thr Thr
 230 235 240 245
 ctg cgt att gcc atg gga caa gta gaa caa gca cta gcc gaa atc aaa 883
 Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys
 250 255 260
 gaa cac ggt acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc 931
 Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser
 265 270 275
 aga tta tat gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag 979
 Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln
 280 285 290
 cac att ttc acc tac aga aaa gga gaa aac aat gag tgacagccaa 1025
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<400> 622

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Phe Ser Pro Leu Ile Ala Arg Ser Ile Glu Glu Ala Gly Phe Glu Gly
 35 40 45

Val Tyr Val Ser Gly Ala Val Ile Ala Ala Asp Leu Ala Leu Pro Asp
 50 55 60

Ile Gly Leu Thr Thr Leu Thr Glu Val Ala His Arg Ala Arg Gln Ile
 65 70 75 80

Ala Arg Val Thr Asp Leu Gly Val Leu Val Asp Ala Asp Thr Gly Phe
85 90 95

Gly Glu Pro Met Ser Ala Ala Arg Thr Val Ala Glu Leu Glu Asp Ala
100 105 110

Gly Val Ala Gly Cys His Leu Glu Asp Gln Val Asn Pro Lys Arg Cys
115 120 125

Gly His Leu Asp Gly Lys Glu Val Val Arg Thr Asp Val Met Val Arg
130 135 140

Arg Ile Ala Ala Ala Val Ser Ala Arg Arg Asp Pro Asn Phe Val Ile
145 150 155 160

Cys Ala Arg Thr Asp Ala Ala Gly Val Glu Gly Ile Asp Ala Ala Ile
165 170 175

Glu Arg Ala Lys Ala Tyr Leu Asp Ala Gly Ala Asp Met Ile Phe Thr
180 185 190

Glu Ala Leu His Ser Glu Ala Asp Phe Arg Tyr Phe Arg His Ala Ile
195 200 205

Pro Asp Ala Leu Leu Leu Ala Asn Met Thr Glu Phe Gly Lys Thr Thr
210 215 220

Leu Leu Ser Ala Asp Val Leu Glu Glu Ile Gly Tyr Asn Ala Val Ile
225 230 235 240

Tyr Pro Val Thr Thr Leu Arg Ile Ala Met Gly Gln Val Glu Gln Ala
245 250 255

Leu Ala Glu Ile Lys Glu His Gly Thr Gln Glu Gly Trp Leu Asp Arg
260 265 270

Met Gln His Arg Ser Arg Leu Tyr Glu Leu Leu Arg Tyr Glu Asp Tyr
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Glu
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 Ala Met Gly Gln Val Glu Gln Ala Leu Ala Glu Ile Lys Glu His Gly
 20 25 30

acc caa gaa gga tgg ctg gac cgc atg caa cac cgc agc aga tta tat 144
 Thr Gln Glu Gly Trp Leu Asp Arg Met Gln His Arg Ser Arg Leu Tyr
 35 40 45

gag ctc ctg cga tac gaa gac tac aac gtc ttt gac cag cac att ttc 192
 Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
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gac 242

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 Met Arg Ile Glu Ile
 1 5

aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr
 10 15 20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr
 25 30 35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu
 40 45 50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly
 55 60 65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val
 70 75 80 85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met
 90 95 100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr
 105 110 115

gta gga aac cta att cag att gtt caa ttg aag cag aac taaccccggtg 500
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gaatgacaaa atc 513

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 20 25 30

Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro
 35 40 45

Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala
 50 55 60

Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe
 65 70 75 80

Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly
 85 90 95

Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala
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Gln Asn
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Met Thr Ser Ile Pro
1 5
aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
10 15 20
cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
25 30 35
gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
40 45 50
gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggc 307
Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
55 60 65
ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
70 75 80 85
gca ggc ttt tca acc gcc gcg gaa tcc aat gcg ttt tat ccg agg aac 403
Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn
90 95 100
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Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr
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cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt 499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly
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atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt 547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
135 140 145
gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
150 155 160 165

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Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
185 190 195	
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Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
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Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
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Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
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Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
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Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
265 270 275	
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Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
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Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
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Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
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Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
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Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
ttc tct gct cgt atc gcc cga aac acc cag ctg ttg ctg cag cag gaa	1267
Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Leu Gln Gln Glu	
375 380 385	
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Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
390 395 400 405	

gag tgg ttg acc aat gag ctg gct aac cgc gcg cgc aag cac atc gat	1363
Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp	
410 415 420	
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Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile	
425 430 435	
cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att	1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile	
440 445 450	
gat tcc ggc cgc cag gcg ctg atc ggc gtg aat cgc tac gtg gcg gaa	1507
Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu	
455 460 465	
gaa gat gag gaa att gaa gtc ctc aag gtt gac aac acc aag gtt cgc	1555
Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg	
470 475 480 485	
gca gaa cag ttg gct aaa ctc gcg caa ctg aaa gca gag cgc aac gat	1603
Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp	
490 495 500	
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Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Arg Asn	
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Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala	
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Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly Glu Ile Ser Asp Ala	
535 540 545	
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Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg	
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Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp Leu Gly Met Asp Val	
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Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu Ala Ala Arg Ala Ala	
630 635 640 645	
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 Phe Gln Asp Leu Tyr Asp Met Gly Ala Ala Ala Ile Tyr Pro Ser Gly
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 710 715 720 725
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 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
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 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65 70 75 80
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
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 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
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 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
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 225 230 235 240
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 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
 260 265 270
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 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
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 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
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 385 390 395 400
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
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 465 470 475 480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
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 580 585 590
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
 595 600 605
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 625 630 635 640
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 675 680 685
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His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
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Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
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Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
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Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe
          135          140          145

gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc 595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly
          150          155          160          165

gct gtg ctg ccg att ctt gcg ttc tat atc gtg gcg gct gag gaa caa 643
Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln
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ggt gtg ggt ccg gag cag ctt gcg ggc acg atc cag aat gac atc ttg 691
Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu
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aaa gaa ttt atg gtg cgc aac acc tat att tat ccg ccg aag ccg tcg 739
Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser
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atg cgc atc att tcc aac atc ttt gag tac acc tcc ttg aag atg cca 787

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Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly	
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gcg	act	gcc	gat	ttg	gag	ctg	gcc	tac	act	ctg	gcg	gat	ggt	att	gaa	883
Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu	
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tac	atc	cgt	gca	ggt	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	931
Tyr	Ile	Arg	Ala	Gly	Lys	Glu	Val	Gly	Leu	Asp	Val	Asp	Lys	Phe	Ala	
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cct	cgt	ctg	tcc	ttc	ttc	tgg	ggt	att	tct	atg	tac	acc	ttc	atg	gag	979
Pro	Arg	Leu	Ser	Phe	Phe	Trp	Gly	Ile	Ser	Met	Tyr	Thr	Phe	Met	Glu	
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Ile	Ala	Lys	Leu	Arg	Ala	Gly	Arg	Leu	Leu	Trp	Ser	Glu	Leu	Val	Ala	
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Lys	Phe	Asp	Pro	Lys	Asn	Ala	Lys	Ser	Gln	Ser	Leu	Arg	Thr	His	Ser	
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cag	acc	tct	ggt	tgg	tcg	ttg	acc	gcg	cag	gat	gtg	tac	aac	aac	gtc	1123
Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val	
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gcc	cgc	acc	gcg	att	gag	gcg	atg	gct	gca	acc	cag	ggc	cac	acc	cag	1171
Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln	
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Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp	
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Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu	
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Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val	
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gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp	
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Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile	
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Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile	
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Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu	

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gag cat aaa gag cca ggg gat ttg gat cag aac ctg ctc aaa ctt gcc Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala 520 525 530			1699
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cgc cca cgt atc ttt att gcc aag atg ggc cag gat gga cat gac cgt Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln Asp Gly His Asp Arg 600 605 610			1939
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<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45
 Glu Ala Gln Ala Ala Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys
 50 55 60
 Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
 65 70 75 80
 Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
 85 90 95
 Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
 100 105 110
 Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
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 Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
 130 135 140
 Met Arg Gln Leu Phe Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser
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 Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
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 Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
 180 185 190
 Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
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 Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
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 Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
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 Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
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 Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
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 Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
 275 280 285
 Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
 290 295 300
 Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
 305 310 315 320
 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp

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Gly	Ser	Tyr	Tyr	Val	Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala
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Arg	Lys	His	Ile	Asp	Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala
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Thr	Ala	Gln	Gly	Ile	Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg
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Thr	Gln	Ala	Arg	Ile	Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn
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Arg	Tyr	Val	Ala	Glu	Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp
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Ala	Glu	Arg	Asn	Asp	Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr
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Ala	Ala	Ala	Arg	Asn	Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn
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Leu	Leu	Lys	Leu	Ala	Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly
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Glu	Ile	Ser	Asp	Ala	Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu
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Ile	Arg	Thr	Leu	Ser	Gly	Val	Tyr	Lys	Asp	Glu	Val	Gly	Lys	Glu	Gly
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Ala	Ala	Arg	Ala	Ala	Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser
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Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr
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Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile Val Thr Thr Pro Asp
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Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala Asp Glu Ser Gln Arg
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gtt gat ggt gaa cgc gtt ggt tgg ggt gtt act gag act ttc gga cat 403
Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr Glu Thr Phe Gly His
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Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu Glu Phe Thr Ala Ala
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Leu Ile His Ala Gly Gly Ser Thr Ser Glu Val Ala Ala Ala Leu Tyr
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Thr Leu Ala Glu Glu Ala Gly Thr Phe Phe Ala Ala Leu Thr Leu Gly	
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Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser Lys Arg Ala Asn Val	
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Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser Asn Gln Gly Ala Ser	
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ctg gga ccg ttg tcc aag cac aat att cgc act ggt ttt act tcc aac 1651
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 505 510 515

ctg ttg gct tcc ggt ggc att gaa gca atc aac ccg ggt caa ctt gtt 1699
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 520 525 530

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 Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
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 165 170 175
 Ala Leu Thr Leu Gly Ser Arg Pro Leu Thr Ala Gln Val Asp Gly Ser
 180 185 190
 His Ser Asp Thr Ile Glu Glu Ala Val Gln Leu Ala Val Asn Ala Ser
 195 200 205
 Lys Arg Ala Asn Val Arg Ala Ile Leu Val Asp Gly Ser Ser Phe Ser
 210 215 220
 Asn Gln Gly Ala Ser Asp Ala Gln Glu Ile Gly Leu Ser Ile Ala Ala
 225 230 235 240
 Gly Val Asp Tyr Val Arg Arg Leu Val Asp Ala Gly Leu Ser Thr Glu
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 Ala Ala Leu Lys Gln Val Ala Phe Arg Phe Ala Val Thr Asp Glu Gln
 260 265 270
 Phe Ala Gln Ile Ser Lys Leu Arg Val Ala Arg Arg Leu Trp Ala Arg
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 Val Cys Glu Val Leu Gly Phe Pro Glu Leu Ala Val Ala Pro Gln His
 290 295 300
 Ala Val Thr Ala Arg Ala Met Phe Ser Gln Arg Asp Pro Trp Val Asn
 305 310 315 320

Met Leu Arg Ser Thr Val Ala Ala Phe Ala Ala Gly Val Gly Gly Ala
 325 330 335
 Thr Asp Val Glu Val Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val
 340 345 350
 Pro Gly Val Ser Arg Asn Phe Ala His Arg Ile Ala Arg Asn Thr Asn
 355 360 365
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 370 375 380
 Gly Gly Ser Tyr Phe Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys
 385 390 395 400
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 405 410 415
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 420 425 430
 Gln Thr Arg Ala Asp Val Ala Ser Arg Lys Lys Lys Leu Thr Gly Ile
 435 440 445
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 450 455 460
 Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
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 Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
 485 490 495
 Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
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 Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
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 Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
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 Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
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<223> RXN00317

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Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
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Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
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Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
                               40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307
Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
                               55 60 65

gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt 355
Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
                               70 75 80 85

tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc cgc ttg aaa tac 403
Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
                               90 95 100

gaa ggt ttc cgt ctg tgc acc gcc acc tcc aag ggc gag ttc ttt gcg 451
Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
                               105 110 115

gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499
Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
                               120 125 130

ggt gcc gcc acc gac agc ggc aac cga cgc agc aaa tct gcc gtg atc 547
Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
                               135 140 145

aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595
Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
                               150 155 160 165

atg att ggt gat cga tca cac gat att gaa ggt tcg agt gaa ttc ggc 643
Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly
                               170 175 180

atc gat tgt gtt gcc gta acc tgg ggc tac ggc agc aaa act gaa tgg 691
Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp

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185 190 195
 gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739
 Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu Glu Leu Glu Arg Ile
 200 205 210
 atc cat gac tgg gcc taaaacttcg ctacctgtgg aaa 777
 Ile His Asp Trp Ala
 215
 <210> 634
 <211> 218
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 634
 Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
 1 5 10 15
 Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
 20 25 30
 His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
 35 40 45
 Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
 50 55 60
 Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65 70 75 80
 Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
 85 90 95
 Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys
 100 105 110
 Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp
 115 120 125
 Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser
 130 135 140
 Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu
 145 150 155 160
 Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly
 165 170 175
 Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly
 180 185 190
 Ser Lys Thr Glu Trp Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu
 195 200 205
 Glu Leu Glu Arg Ile Ile His Asp Trp Ala
 210 215

<210> 635

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<211> 439
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(439)
<223> FRXA00317
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gtcaagccaa gccttgaaaa attctggcaa ggtaaatggt																
											gtg	act	acg	cct	tct	115
											Val	Thr	Thr	Pro	Ser	
											1				5	
aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc																163
Lys	Lys	Thr	Leu	Leu	Phe	Asp	Leu	Asp	Gly	Thr	Leu	Val	Asp	Ser	Phe	
					10				15					20		
ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg																211
Pro	Gly	Ile	Arg	Thr	Ser	Phe	Leu	His	Thr	Leu	His	Glu	Lys	Asn	Trp	
			25					30						35		
gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg																259
Glu	Ile	Pro	Ser	Glu	Glu	Arg	Ile	Ser	Gln	Val	Pro	Gly	Pro	Pro	Met	
		40					45					50				
gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac																307
Glu	Trp	Thr	Phe	Gln	Asp	Leu	Gly	Met	Thr	Pro	Glu	Gln	Ala	Gln	Asp	
	55					60					65					
gct ctg cag acc tac ctt gag cat tac ggc cag gtg ggt tgg gat ctt																355
Ala	Leu	Gln	Thr	Tyr	Leu	Glu	His	Tyr	Gly	Gln	Val	Gly	Trp	Asp	Leu	
70					75					80					85	
tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc ccc ttg ata tac																403
Ser	Glu	Ala	Phe	Pro	Gly	Met	Arg	Asp	Leu	Leu	Ile	Pro	Leu	Ile	Tyr	
				90					95					100		
gaa ggt ttt cgt ctg tgc acc gcc acc ttt caa ggg																439
Glu	Gly	Phe	Arg	Leu	Cys	Thr	Ala	Thr	Phe	Gln	Gly					
			105					110								

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<210> 636
<211> 113
<212> PRT
<213> Corynebacterium glutamicum
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<400> 636
Val Thr Thr Pro Ser Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr
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Leu Val Asp Ser Phe Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu
          20          25          30
His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
          35          40          45
Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro

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<400> 637																		
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gcacattgca gatcgtgccca ctttaactaa ggttgacggc																		
atg att aag gcg att																		115
Met Ile Lys Ala Ile																		
1 5																		
ttc tgg gac atg gac ggc acg atg gtg gac tct gag cca cag tgg ggc																		163
Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser Glu Pro Gln Trp Gly																		
10 15 20																		
att gct acc tac gag ctc agc gaa gcc atg ggc cgc cgc ctc acc ccg																		211
Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro																		
25 30 35																		
gag ctc cgg gaa ctc acc gtc ggc tgc agc ctg ccg cgc acc atg cgc																		259
Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu Pro Arg Thr Met Arg																		
40 45 50																		
tta tgc gca gag cac gca ggc att aca ttg agc gac gcg gac tac gag																		307
Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser Asp Ala Asp Tyr Glu																		
55 60 65																		
cgc tac cgg gct ggc atg ttc gcc cgg gtc cat gag ctt ttc gac gaa																		355
Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu																		
70 75 80 85																		
tcc ctc gtc cca aat cca ggc gtc acc gaa ctc ctg aca gag ttg aag																		403
Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu Leu Thr Glu Leu Lys																		
90 95 100																		
gcc ctc gag atc ccc atg ttg gtc acc acc aac aca gag cgc gat ctc																		451
Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn Thr Glu Arg Asp Leu																		
105 110 115																		
gcg acc cgt tca gtc gca gcc gtg gga aat gag ttc ttc atc ggt tct																		499

Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
 120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547
 Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
 135 140 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg 595
 Leu Glu Ala Ala Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
 150 155 160 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643
 Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
 170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691
 Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
 185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739
 Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
 200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787
 Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile Glu Pro Ala Gly Val
 215 220 225

gca aaa taaaaccagg tgggggagtg aaa 816
 Ala Lys
 230

<210> 638

<211> 231

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

Met Ile Lys Ala Ile Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser
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Glu Pro Gln Trp Gly Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly
 20 25 30

Arg Arg Leu Thr Pro Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu
 35 40 45

Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser
 50 55 60

Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His
 65 70 75 80

Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu
 85 90 95

Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn
 100 105 110

Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu
 115 120 125

Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro
 130 135 140
 Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro
 145 150 155 160
 Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala
 165 170 175
 Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln
 180 185 190
 Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser
 195 200 205
 Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile
 210 215 220
 Glu Pro Ala Gly Val Ala Lys
 225 230

<210> 639
 <211> 531
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(508)
 <223> RXN02461

<400> 639
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 acgactatta tgtcacgaag aaaccaaaga aagggaata atg cgc gga cta att 115
 Met Arg Gly Leu Ile
 1 5
 gtt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163
 Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
 10 15 20
 tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211
 Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
 25 30 35
 atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
 Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
 40 45 50
 ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
 Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
 55 60 65
 ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
 Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
 70 75 80 85
 atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc 403

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Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
      90                      95                      100

aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag 451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
      105                      110                      115

caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa 499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
      120                      125                      130

gga gaa ttc taatcttgcg cgtctacatc cca 531
Gly Glu Phe
      135

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<210> 640
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 640
Met Arg Gly Leu Ile Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp
  1              5              10              15

Glu Asp Gln Arg Arg Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn
      20              25              30

Gly Val Gly Thr Val Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala
      35              40              45

Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
      50              55              60

Leu Ser Gly Glu Leu Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln
      65              70              75              80

Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
      85              90              95

Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
      100             105             110

Gly Val Tyr Tyr Gln Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly
      115             120             125

Leu Phe Gly Leu Glu Gly Glu Phe
      130             135

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<210> 641
 <211> 1662
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1639)
 <223> RXN01744

<400> 641

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gttctctgtca acctgcaatg gaagaggaag tgtacctagc																	115
gtg gat gtc gtc gac Val Asp Val Val Asp 1 5																	
atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt																	163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe 10 15 20																	
gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg																	211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr 25 30 35																	
ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt																	259
Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe 40 45 50																	
ttt ggc act gtg ctg ctc atc aac ttc gcg gtt ggt gta gca acg ggc																	307
Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly 55 60 65																	
att gtg cag gag ttc cag ttc ggt atg aac tgg tcg gaa tat tcg cgt																	355
Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg 70 75 80 85																	
ttc gtc ggt gat gtt ttc ggc gga ccg ctg gct ttg gag ggt ctt atc																	403
Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala Leu Glu Gly Leu Ile 90 95 100																	
gcg ttc ttc ctt gag tct gta ttc ctg gga ctg tgg att ttc gga tgg																	451
Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu Trp Ile Phe Gly Trp 105 110 115																	
ggg aag att cct ggt tgg ttg cac act gca tcc att tgg atc gtt gct																	499
Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser Ile Trp Ile Val Ala 120 125 130																	
att gcg acg aat att tct gcc tat ttc atc atc gtg gcc aac tcg ttt																	547
Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile Val Ala Asn Ser Phe 135 140 145																	
atg cag cat ccg gtg ggt gct gag tat aac cct gag act ggt cgt gcg																	595
Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro Glu Thr Gly Arg Ala 150 155 160 165																	
gag ctt act gat ttt tgg gct ctt ctc aca aac tcc acc gcg ctg gct																	643
Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn Ser Thr Ala Leu Ala 170 175 180																	
gcg ttc ccg cat gct gtt gcc ggt ggt ttt tta aca gct gga act ttc																	691
Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu Thr Ala Gly Thr Phe 185 190 195																	
gtt ctc gga att tcg ggt tgg tgg att att cgt gcg cac cgt cag gcc																	739
Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg Ala His Arg Gln Ala 200 205 210																	
aag aag gct gag tcg gaa atc gag tcg aag cat tcg atg cac agg ccc																	787
Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His Ser Met His Arg Pro 215 220 225																	

gcg ttg tgg gtt ggt tgg tgg acc aca gtt gtc tct tcc gtg gcg ctg	835
Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val Ser Ser Val Ala Leu	
230 235 240 245	
ttc atc act ggc gat atc cag gcg aag ctc atg ttc gtg caa cag cca	883
Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met Phe Val Gln Gln Pro	
250 255 260	
atg aag atg gcg tgc gcg gaa tcc ttg tgt gaa acc gcc aca gat cca	931
Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu Thr Ala Thr Asp Pro	
265 270 275	
aac ttc tcc att ctg aca att ggt acg cac aac aac tgc gat acg gta	979
Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn Asn Cys Asp Thr Val	
280 285 290	
acc cac ctg atc gat gtt ccg ttt gtg ctt cca ttc ttg gct gaa gga	1027
Thr His Leu Ile Asp Val Pro Phe Val Leu Pro Phe Leu Ala Glu Gly	
295 300 305	
aaa ttc acc ggt gtg act ttg cag ggt gta aac cag ctc caa gct gca	1075
Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn Gln Leu Gln Ala Ala	
310 315 320 325	
gcg gag caa gca tac ggt cct ggc aac tac tcc cct aac ttg ttt gtc	1123
Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser Pro Asn Leu Phe Val	
330 335 340	
acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg	1171
Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu	
345 350 355	
gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca	1219
Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro	
360 365 370	
act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc	1267
Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile	
375 380 385	
ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg	1315
Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met	
390 395 400 405	
ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc ggc gat	1363
Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp	
410 415 420	
gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat	1411
Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp	
425 430 435	
cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc	1459
His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu	
440 445 450	
tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt	1507
Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val	
455 460 465	

ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act 1555
 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr
 470 475 480 485

gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa 1603
 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln
 490 495 500

ttt act gcc gct gcc cca acc aca ggt gaa aag gaa taaccatgga 1649
 Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys Glu
 505 510

tctcaatacc ttt 1662

<210> 642
 <211> 513
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 642
 Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
 1 5 10 15
 Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
 20 25 30
 Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr
 35 40 45
 Arg Ala Thr Arg Phe Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val
 50 55 60
 Gly Val Ala Thr Gly Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp
 65 70 75 80
 Ser Glu Tyr Ser Arg Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala
 85 90 95
 Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly Leu
 100 105 110
 Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala Ser
 115 120 125
 Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile Ile
 130 135 140
 Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn Pro
 145 150 155 160
 Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr Asn
 165 170 175
 Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe Leu
 180 185 190
 Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile Arg
 195 200 205
 Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys His

210	215	220
Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val Val 225 230 235 240		
Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu Met 245 250 255		
Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys Glu 260 265 270		
Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His Asn 275 280 285		
Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu Pro 290 295 300		
Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val Asn 305 310 315 320		
Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr Ser 325 330 335		
Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu 340 345 350		
Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg 355 360 365		
Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly 370 375 380		
Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp 385 390 395 400		
Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro 405 410 415		
Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp 420 425 430		
Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile 435 440 445		
Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu 450 455 460		
Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser 465 470 475 480		
Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro 485 490 495		
Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys 500 505 510		

Glu

<210> 643

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<211> 238
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(238)  
<223> FRXA00055
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<400> 643
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gttcctgtca acctgcaatg gaagaggaag tgtacctagc gtg gat gtc gtc gac 115
Val Asp Val Val Asp
1 5

atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
10 15 20

gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211
Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
25 30 35

ttt tgg caa gtt acc ggc aaa gag cac 238
Phe Trp Gln Val Thr Gly Lys Glu His
40 45

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<210> 644
<211> 46
<212> PRT
<213> Corynebacterium glutamicum
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Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
  1             5             10             15
Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
      20             25             30
Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
      35             40             45

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<210> 645
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<212> DNA
<213> Corynebacterium glutamicum
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<222> (1)..(1302)
<223> FRXA01744
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Trp	Ser	Glu	Tyr	Ser	Arg	Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu	
1				5				10						15		
gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga																96

Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly		
			20					25					30				
ctg	tgg	att	ttc	gga	tgg	ggg	aag	att	cct	ggg	tgg	ttg	cac	act	gca	144	
Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala		
		35					40					45					
tcc	att	tgg	atc	gtt	gct	att	gcg	acg	aat	att	tct	gcc	tat	ttc	atc	192	
Ser	Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile		
		50				55					60						
atc	gtg	gcc	aac	tcg	ttt	atg	cag	cat	ccg	gtg	ggg	gct	gag	tat	aac	240	
Ile	Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn		
		65			70				75						80		
cct	gag	act	ggg	cgt	gcg	gag	ctt	act	gat	ttt	tgg	gct	ctt	ctc	aca	288	
Pro	Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr		
			85						90					95			
aac	tcc	acc	gcg	ctg	gct	gcg	ttc	ccg	cat	gct	gtt	gcc	ggg	ggg	ttt	336	
Asn	Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe		
			100					105					110				
tta	aca	gct	gga	act	ttc	gtt	ctc	gga	att	tcg	ggg	tgg	tgg	att	att	384	
Leu	Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile		
		115				120						125					
cgt	gcg	cac	cgt	cag	gcc	aag	aag	gct	gag	tcg	gaa	atc	gag	tcg	aag	432	
Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys		
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cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggg	tgg	tgg	acc	aca	gtt	480	
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val		
		145			150					155					160		
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528	
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu		
			165						170					175			
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576	
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys		
			180					185					190				
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggg	acg	cac	624	
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His		
		195				200						205					
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672	
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu		
		210				215					220						
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggg	gtg	act	ttg	cag	ggg	gta	720	
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val		
		225			230					235					240		
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggg	cct	ggc	aac	tac	768	
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr		
			245					250						255			
tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816	
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly		

260	265	270	
ctg atg ctt ggt tct ttg gct atc gct gcg att gcg tgg ctg ttg ctg			864
Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu			
275	280	285	
cgt aag aag cgc aca cca act gga aag att gct cgt ctg ttc cag atc			912
Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile			
290	295	300	
ggc agc ctc att gct atc ccg ttc cca ttc ttg gcc aac tct gct ggt			960
Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly			
305	310	315	320
tgg atc ttc acc gag atg ggc cgc cag cct tgg gtg gtg cac ccg aac			1008
Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn			
325	330	335	
cct gaa tct gcc ggc gat gcc cga aca gag atg atc cgg atg act gtt			1056
Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val			
340	345	350	
gat atg ggt gta tct gat cat gcg cca tgg caa gtc tgg ctg act ctc			1104
Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu			
355	360	365	
att ggc ttc acg att ctc tat ctc att ttg ttc gtg gtg tgg gtg tgg			1152
Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp			
370	375	380	
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca			1200
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro			
385	390	395	400
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg			1248
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met			
405	410	415	
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa			1296
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu			
420	425	430	
aag gaa taaccatgga tctcaatacc ttt			1325
Lys Glu			

<210> 646

<211> 434

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

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Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly
		20						25					30		

Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala
		35					40					45			

Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
 50 55 60
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
 65 70 75 80
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
 85 90 95
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
 100 105 110
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
 115 120 125
 Arg Ala His Arg Gln Ala Lys Lys Ala Glu Ser Glu Ile Glu Ser Lys
 130 135 140
 His Ser Met His Arg Pro Ala Leu Trp Val Gly Trp Trp Thr Thr Val
 145 150 155 160
 Val Ser Ser Val Ala Leu Phe Ile Thr Gly Asp Ile Gln Ala Lys Leu
 165 170 175
 Met Phe Val Gln Gln Pro Met Lys Met Ala Ser Ala Glu Ser Leu Cys
 180 185 190
 Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
 195 200 205
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
 210 215 220
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
 225 230 235 240
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
 245 250 255
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
 260 265 270
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
 275 280 285
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
 290 295 300
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
 305 310 315 320
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
 325 330 335
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
 340 345 350
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
 355 360 365

Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
 370 375 380

Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
 385 390 395 400

Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
 405 410 415

Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
 420 425 430

Lys Glu

<210> 647
 <211> 307
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(307)
 <223> RXA00379

<400> 647
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tgtgttggat gttgcgttgc cattggtaga tgaggcctaa atg tct gag att gtg 115
 Met Ser Glu Ile Val
 1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
 10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
 Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser
 25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
 Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
 40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
 55 60 65

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 <211> 69
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 648
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Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
 20 25 30

Leu Gly Gly Val Phe Ala Leu Gly Trp Thr Pro Cys Leu Gly Pro Thr
 1 5 10 15
 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala
 20 25 30
 Ala Arg Gly Val Ile Leu Ile Val Gly Tyr Cys Leu Gly Leu Gly Leu
 35 40 45
 Pro Phe Leu Leu Ile Ala Leu Gly Ser Ser Lys Ala Leu Thr Gly Val
 50 55 60
 Glu Trp Leu Arg Lys His Ser Arg Thr Leu Gln Ile Ile Gly Gly Val
 65 70 75 80
 Phe Leu Ile Leu Val Gly Val Ala Leu Leu Ser Gly Ser Trp Ala Ile
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 Phe Ile Asn Trp Val Arg Gln Trp Thr Val Glu Tyr Gly Ala Thr Leu
 100 105 110

Leu

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01743

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 Met Asp Leu Asn Thr
 1 5
 ttt tgg ttt att ctc atc gca ttt ttg ttt gcg gga tac ttt ctc ctc 163
 Phe Trp Phe Ile Leu Ile Ala Phe Leu Phe Ala Gly Tyr Phe Leu Leu
 10 15 20
 gaa gga ttc gac ttc ggc gtc gga att ttg gca ccc atc atc ggt aaa 211
 Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala Pro Ile Ile Gly Lys
 25 30 35
 gat tca gcg gct agg aac aca gtg atc cgt acg att ggc cct gtc tgg 259
 Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr Ile Gly Pro Val Trp
 40 45 50
 gac gga aat gaa gtg tgg ctg atc gtg gca ggt ggc gct ttg ttt gct 307
 Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly Gly Ala Leu Phe Ala
 55 60 65
 gcc ttc cct gag tgg tac gca acg atg ttc tcc gga atg tat ctg ccg 355
 Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser Gly Met Tyr Leu Pro
 70 75 80 85

ctg ttc ctc gtg ctt gtg tcg ttg atc atg cgc gtg gtg ggc ctt gaa 403
 Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg Val Val Gly Leu Glu
 90 95 100

tgg cgc aag aaa gtc gat gat cct cgt tgg caa aag tgg tct gac cgg 451
 Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln Lys Trp Ser Asp Arg
 105 110 115

gcc atc ttt att ggt tct tgg act cca ccg ctg atg tgg gga ttc atc 499
 Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu Met Trp Gly Phe Ile
 120 125 130

ttc gcc aat att ttg cgt ggc atg ccc ctc aag gcg gat cac acc atc 547
 Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys Ala Asp His Thr Ile
 135 140 145

gat gct gcg gca gcc ctt cct ggc atg gtc aac gtc ttc gcc att ctg 595
 Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn Val Phe Ala Ile Leu
 150 155 160 165

ggt gca ctt gcg ttc acc gca ctg ttc gcc ctt cat ggt ctc gca ttc 643
 Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu His Gly Leu Ala Phe
 170 175 180

atc cgc ctg aaa act gct ggt cgg gtg cgc acc gat gcg gcg aag gca 691
 Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala
 185 190 195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val
 200 205 210

ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca 787
 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala
 215 220 225

gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys
 230 235 240 245

gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883
 Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly
 250 255 260

gtc gtt gca ctg ctg ttt 901
 Val Val Ala Leu Leu Phe
 265

<210> 652
 <211> 267
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 652
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 Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala
 20 25 30

Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr
 35 40 45
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly
 50 55 60
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser
 65 70 75 80
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg
 85 90 95
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln
 100 105 110
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu
 115 120 125
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys
 130 135 140
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn
 145 150 155 160
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu
 165 170 175
 His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr
 180 185 190
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr
 195 200 205
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp
 210 215 220
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala
 225 230 235 240
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser
 245 250 255
 Val Ala Val Ile Gly Val Val Ala Leu Leu Phe
 260 265

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<211> 1779

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1756)

<223> RXN02480

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															Met	Thr	Thr	Thr	Asp	
															1				5	
cac	aag	cag	ctg	ggc	att	atg	tac	atc	att	atg	tcc	ttc	agc	ttc	ttc	163				
His	Lys	Gln	Leu	Gly	Ile	Met	Tyr	Ile	Ile	Met	Ser	Phe	Ser	Phe	Phe					
				10					15					20						
ttc	ctc	ggt	ggc	ttg	atg	gcc	ctg	ctt	atc	cga	gcg	gag	ctt	ttc	acc	211				
Phe	Leu	Gly	Gly	Leu	Met	Ala	Leu	Leu	Ile	Arg	Ala	Glu	Leu	Phe	Thr					
				25					30					35						
cct	ggt	ctg	cag	ttc	ctg	tct	aat	gag	cag	ttc	aac	cag	ctg	ttc	acc	259				
Pro	Gly	Leu	Gln	Phe	Leu	Ser	Asn	Glu	Gln	Phe	Asn	Gln	Leu	Phe	Thr					
				40					45					50						
atg	cac	gga	act	gtc	atg	ctg	ctg	ctg	tac	gga	act	cca	att	gtt	tgg	307				
Met	His	Gly	Thr	Val	Met	Leu	Leu	Leu	Tyr	Gly	Thr	Pro	Ile	Val	Trp					
				55					60					65						
ggt	ttt	gct	aac	tac	gtc	ctg	cca	ctt	cag	atc	ggt	gcg	cct	gac	gta	355				
Gly	Phe	Ala	Asn	Tyr	Val	Leu	Pro	Leu	Gln	Ile	Gly	Ala	Pro	Asp	Val					
				70					75					80						
gct	ttc	cca	cgt	ttg	aat	gct	ttc	ggc	ttc	tgg	atc	acc	acc	gtc	ggt	403				
Ala	Phe	Pro	Arg	Leu	Asn	Ala	Phe	Gly	Phe	Trp	Ile	Thr	Thr	Val	Gly					
				90					95					100						
ggt	gtc	gcg	atg	ctg	acc	ggc	ttc	ctg	acc	ccg	ggt	ggt	gct	gcc	gac	451				
Gly	Val	Ala	Met	Leu	Thr	Gly	Phe	Leu	Thr	Pro	Gly	Gly	Ala	Ala	Asp					
				105					110					115						
ttc	ggt	tgg	acc	atg	tac	tcc	cca	ctg	tct	gac	gca	att	cac	tcc	cca	499				
Phe	Gly	Trp	Thr	Met	Tyr	Ser	Pro	Leu	Ser	Asp	Ala	Ile	His	Ser	Pro					
				120					125					130						
ggc	ctt	ggc	tct	gac	atg	tgg	att	gtc	ggt	gtc	ggt	gca	act	ggt	att	547				
Gly	Leu	Gly	Ser	Asp	Met	Trp	Ile	Val	Gly	Val	Gly	Ala	Thr	Gly	Ile					
				135					140					145						
ggc	tcc	gtt	gct	tcc	gca	att	aac	atg	ctc	acc	acc	atc	ctc	tgc	ctc	595				
Gly	Ser	Val	Ala	Ser	Ala	Ile	Asn	Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu					
				150					155					160						
cgc	gca	cct	ggt	atg	acc	atg	ttc	cgt	atg	cct	att	ttc	acc	tgg	aat	643				
Arg	Ala	Pro	Gly	Met	Thr	Met	Phe	Arg	Met	Pro	Ile	Phe	Thr	Trp	Asn					
				170					175					180						
atc	ttc	gtt	gtt	tcc	gtt	ctt	gct	ctg	ctg	atc	ttc	cca	ctg	ctg	ctc	691				
Ile	Phe	Val	Val	Ser	Val	Leu	Ala	Leu	Leu	Ile	Phe	Pro	Leu	Leu	Leu					
				185					190					195						
gct	gct	gca	ctg	ggt	gtt	ctg	tat	gac	cgc	aag	ctt	ggt	gga	cac	ctg	739				
Ala	Ala	Ala	Leu	Gly	Val	Leu	Tyr	Asp	Arg	Lys	Leu	Gly	Gly	His	Leu					
				200					205					210						
tac	gat	cca	gct	aac	ggc	ggc	tcc	ctc	ctg	tgg	cag	cac	ctg	ttc	tgg	787				
Tyr	Asp	Pro	Ala	Asn	Gly	Gly	Ser	Leu	Leu	Trp	Gln	His	Leu	Phe	Trp					
				215					220					225						
ttc	ttc	gga	cac	cct	gag	gtt	tac	gtt	ctg	gcg	ctg	ccg	ttc	ttc	ggc	835				
Phe	Phe	Gly	His	Pro	Glu	Val	Tyr	Val	Leu	Ala	Leu	Pro	Phe	Phe	Gly					

230	235	240	245	
att gtt tct gag Ile Val Ser Glu	atc att cct gtg ttc tcc cgt aag cca atg ttc ggt Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly			883
	250	255	260	
tac gtc ggc ctg Tyr Val Gly Leu	atc ttc gca acc ttg tcc att ggt gca ctg tcc atg Ile Phe Ala Thr Leu Ser Ile Gly Ala Leu Ser Met			931
	265	270	275	
gct gtg tgg gct Ala Val Trp Ala	cac cac atg ttc gtt act ggc gca gtt ttg ctt ccg His His Met Phe Val Thr Gly Ala Val Leu Leu Pro			979
	280	285	290	
ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc ggc gtt aag Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr Gly Val Lys				1027
	295	300	305	
ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc act tgg gaa Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile Thr Trp Glu				1075
	310	315	320	325
acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc ctc ttc ggt Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe Leu Phe Gly				1123
	330	335	340	
ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac ttc cac ttg Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp Phe His Leu				1171
	345	350	355	
gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc ctc ttc ggt Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr Leu Phe Gly				1219
	360	365	370	
acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg ttc ccg aag Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp Phe Pro Lys				1267
	375	380	385	
atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc cac ttc tgg Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile His Phe Trp				1315
	390	395	400	405
ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag cac tgg gtg Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln His Trp Val				1363
	410	415	420	
ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg gat tct gat Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu Asp Ser Asp				1411
	425	430	435	
ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac ttc ctg ctt Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr Phe Leu Leu				1459
	440	445	450	
ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag tcc tgg cgc Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys Ser Trp Arg				1507
	455	460	465	
tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac ggc aac tcc Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr Gly Asn Ser				1555
	470	475	480	485

ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac ttc gca tcc 1603
 Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn Phe Ala Ser
 490 495 500

ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg cac tac ccg 1651
 Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu His Tyr Pro
 505 510 515

cac atg att gaa cgc atg cgc gca gag gca cac act gga cat cac gat 1699
 His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly His His Asp
 520 525 530

gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt gca tct gac 1747
 Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu Ala Ser Asp
 535 540 545

tcc agc cgc taaaagcgtc tgatttaagt cgg 1779
 Ser Ser Arg
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<210> 654

<211> 552

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 654

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Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
 20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
 35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
 50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile
 65 70 75 80

Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp
 85 90 95

Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro
 100 105 110

Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp
 115 120 125

Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val
 130 135 140

Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr
 145 150 155 160

Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro
 165 170 175

Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile
 180 185 190
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys
 195 200 205
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp
 210 215 220
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala
 225 230 235 240
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg
 245 250 255
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile
 260 265 270
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly
 275 280 285
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val
 290 295 300
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly
 305 310 315 320
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala
 325 330 335
 Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro
 340 345 350
 Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His
 355 360 365
 Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr
 370 375 380
 Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly
 385 390 395 400
 Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu
 405 410 415
 Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp
 420 425 430
 Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val
 435 440 445
 Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val
 450 455 460
 Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp
 465 470 475 480
 Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg
 485 490 495
 His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe

500 505 510
 Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His
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 Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro
 530 535 540
 Ala Leu Ala Ser Asp Ser Ser Arg
 545 550

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 <211> 385
 <212> DNA
 <213> Corynebacterium glutamicum

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 <221> CDS
 <222> (101)..(385)
 <223> FRXA01919

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 gacaggccat gcacgcaagg gcagcaaagc atgggtaatg atg acc acc acc gac 115
 Met Thr Thr Thr Asp
 1 5
 cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
 10 15 20
 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
 25 30 35
 cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
 40 45 50
 atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
 55 60 65
 ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe
 70 75 80 85
 tct aaa acc cgg gtg aac tct ccc agg gag 385
 Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
 90 95

<210> 656
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 656
 Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met

1	5	10	15
Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg	20	25	30
Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe	35	40	45
Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly	50	55	60
Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr	65	70	75
Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu	85	90	95

<210> 657

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(949)

<223> FRXA02480

<400> 657

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aagccaatgt tcgggttacg tcggcctgat cttcgcaacc ttg tcc att ggt gca 115
                                   Leu Ser Ile Gly Ala
                                   1 5
ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163
Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val
                                   10 15 20
ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
                                   25 30 35
ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259
Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile
                                   40 45 50
act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
                                   55 60 65
ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355
Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp
                                   70 75 80 85
ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403
Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr
                                   90 95 100
ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg 451
Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp

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105	110	115	
ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc			499
Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile			
120	125	130	
cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag			547
His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln			
135	140	145	
cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg			595
His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu			
150	155	160	165
gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac			643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr			
170	175	180	
ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag			691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys			
185	190	195	
tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac			739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr			
200	205	210	
ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac			787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn			
215	220	225	
ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg			835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu			
230	235	240	245
cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga			883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly			
250	255	260	
cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt			931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu			
265	270	275	
gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg			972
Ala Ser Asp Ser Ser Arg			
280			

<210> 658

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe
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Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met
 35 40 45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly
 50 55 60
 Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala
 65 70 75 80
 Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala
 85 90 95
 His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala
 100 105 110
 Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu
 115 120 125
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly
 130 135 140
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg
 145 150 155 160
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile
 165 170 175
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile
 180 185 190
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp
 195 200 205
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro
 210 215 220
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg
 225 230 235 240
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala
 245 250 255
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly
 260 265 270
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg
 275 280

<210> 659

<211> 735

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(712)

<223> FRXA02481

<400> 659

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tgctttcggc ttctgaatca ccaccgtcgg tgggtgcgcg atg ctg acc ggc ttc 115

	Met	Leu	Thr	Gly	Phe	
	1				5	
cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac						163
Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His						
				10	15	20
tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg						211
Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu						
				25	30	35
tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac						259
Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn						
				40	45	50
atg ctc acc acc atc ctc tgc ctc cgc gca cct ggt atg acc atg ttc						307
Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe						
				55	60	65
cgt atg cct att ttc acc tgg aat atc ttc gtt gtt tcc gtt ctt gct						355
Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala						
				70	75	80
ctg ctg atc ttc cca ctg ctg ctc gct gct gca ctg ggt gtt ctg tat						403
Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Leu Gly Val Leu Tyr						
				90	95	100
gac cgc aag ctt ggt gga cac ctg tac gat cca gct aac ggc ggc tcc						451
Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser						
				105	110	115
ctc ctg tgg cag cac ctg ttc tgg ttc ttc gga cac cct gag gtt tac						499
Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr						
				120	125	130
gtt ctg gcg ctg ccg ttc ttc ggc att gtt tct gag atc att cct gtg						547
Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val						
				135	140	145
ttc tcc cgt aag cca atg ttc ggg tta cgt cgg cct gat ctt cgc aac						595
Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg Pro Asp Leu Arg Asn						
				150	155	160
ctt gtc cat tgg tgc act gtc cat ggc tgt gtg ggc tca cca cat gtt						643
Leu Val His Trp Cys Thr Val His Gly Cys Val Gly Ser Pro His Val						
				170	175	180
cgt tac tgg cgc agt ttt gct tcc gtt ctt ctc ctt cat gac gtt cct						691
Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu Leu His Asp Val Pro						
				185	190	195
gat ttc ggt tcc tac cgg cgt taagttcttc aactgggttg gaa						735
Asp Phe Gly Ser Tyr Arg Arg						
				200		

<210> 660

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met Leu Thr Gly Phe Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly
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Pro Cys Thr Pro His Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val
 20 25 30

Leu Thr Cys Gly Leu Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val
 35 40 45

Ala Ser Ala Ile Asn Met Leu Thr Thr Ile Leu Cys Leu Arg Ala Pro
 50 55 60

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
 65 70 75 80

Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
 85 90 95

Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
 100 105 110

Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
 115 120 125

His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
 130 135 140

Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg
 145 150 155 160

Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
 165 170 175

Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
 180 185 190

Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
 195 200

<210> 661

<211> 1200

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1177)

<223> RXA02140

<400> 661

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aggtctctgg tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115
 Val Glu Gln Gln Asn
 1 5

aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta 163
 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu
 10 15 20

ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg	211
Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val	
25 30 35	
ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa	259
Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu	
40 45 50	
gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg	307
Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp	
55 60 65	
atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc	355
Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala	
70 75 80 85	
tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag	403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys	
90 95 100	
cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg	451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro	
105 110 115	
atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac	499
Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp	
120 125 130	
aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc	547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr	
135 140 145	
gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca	595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser	
150 155 160 165	
ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag	643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln	
170 175 180	
gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att	691
Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile	
185 190 195	
cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att	739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile	
200 205 210	
gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg	787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val	
215 220 225	
aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc	835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser	
230 235 240 245	
ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct	883
Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro	
250 255 260	

gag gca aac aag tcc cag cgt gtc ttc cag att gaa gag atc act gag 931
 Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu
 265 270 275
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 Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His
 280 285 290
 gca atg atg aac ttc gag ctt cgt gtc gtc gat cgc gat tcc ttc gct 1027
 Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala
 295 300 305
 gag tac atc agc ttc cgt gac tcc aac cca gac gca acc aac gct cag 1075
 Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln
 310 315 320 325
 gca ctt gag cac att ggt caa gct cct tac gct act tcc act agc cca 1123
 Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro
 330 335 340
 ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc 1171
 Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser
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<210> 662

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

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 35 40 45
 Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val
 50 55 60
 Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu
 65 70 75 80
 Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu
 85 90 95
 Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val
 100 105 110
 Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr
 115 120 125
 Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val
 130 135 140

Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser
 145 150 155 160
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser
 165 170 175
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser
 180 185 190
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu
 195 200 205
 Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val
 210 215 220
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala
 225 230 235 240
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp
 245 250 255
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile
 260 265 270
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met
 275 280 285
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp
 290 295 300
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp
 305 310 315 320
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala
 325 330 335
 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly
 340 345 350
 Glu Asn Thr Gln Ser Asn Ala
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<210> 663
 <211> 774
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(751)
 <223> RXA02142

<400> 663
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 aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115
 Val Thr Leu Ala Asn
 1 5

caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt 163
 Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly
 10 15 20

atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc 211
 Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val
 25 30 35

agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc 259
 Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala
 40 45 50

ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat 307
 Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn
 55 60 65

gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg 355
 Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu
 70 75 80 85

ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga 403
 Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val Thr Cys Gln Phe Gly
 90 95 100

gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc 451
 Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe
 105 110 115

ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga'cag ggc tac 499
 Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr
 120 125 130

gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc 547
 Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val
 135 140 145

tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg 595
 Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val
 150 155 160 165

atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag 643
 Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys
 170 175 180

tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat 691
 Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr
 185 190 195

tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att 739
 Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile
 200 205 210

tac ttc att cag taggcagtaa ggaatcctca acg 774
 Tyr Phe Ile Gln
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<210> 664

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala
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Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn
 20 25 30

Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu
 35 40 45

Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala
 50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn
 65 70 75 80

Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val
 85 90 95

Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
 100 105 110

Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val
 115 120 125

Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr
 130 135 140

Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe
 145 150 155 160

His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu
 165 170 175

Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala
 180 185 190

Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly
 195 200 205

Leu Phe Ile Thr Ile Tyr Phe Ile Gln
 210 215

<210> 665

<211> 1347

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1324)

<223> RXA02144

<400> 665

actcactcgg tagcttgggc ccagtggtg aggggtctgtt catgtgggta ttcggcatct 60

tggtcctcgt ggccgccgct atgtggattg gatcacgttc atg agt aac aac aac 115
 Met Ser Asn Asn Asn
 1 5

gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat	163
Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp	
10 15 20	
ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc	211
Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg	
25 30 35	
aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca	259
Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala	
40 45 50	
cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg	307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat	547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga	595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca	643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg	787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt	835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	

tcc cgc ctg gtt cgt atg cgc cca gaa gat ctg gca gca gca tcc atg 883
 Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met
 250 255 260

 gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa 931
 Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu
 265 270 275

 tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac 979
 Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His
 280 285 290

 ggc cca cgc aac gca gtt atg ttg atc cgt ctc cgt acc gct gac gct 1027
 Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala
 295 300 305

 gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac 1075
 Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp
 310 315 320 325

 tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca 1123
 Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser
 330 335 340

 ctg tac gag gct cag acc aat cgt att ctg tgc cca tgt cac cag tcg 1171
 Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser
 345 350 355

 cag ttt gac gca ttg cac tac gga aag cca gtc ttt gga cct gct gcc 1219
 Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala
 360 365 370

 cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc 1267
 Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu
 375 380 385

 atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag 1315
 Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu
 390 395 400 405

 cgt aag tca tgagtctagc taccgtggga aac 1347
 Arg Lys Ser

<210> 666

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
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Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
 20 25 30

Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala
 35 40 45

Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile

50					55					60					
Ile	Gly	Gly	Leu	Gly	Phe	Leu	Ala	Thr	Tyr	Ile	Phe	Trp	Pro	Trp	Glu
65					70					75					80
Tyr	Lys	Ala	His	Gly	Asp	Glu	Gly	Leu	Leu	Ala	Tyr	Thr	Leu	Tyr	Thr
				85					90					95	
Pro	Met	Leu	Gly	Ile	Thr	Ser	Gly	Leu	Cys	Ile	Leu	Ser	Leu	Gly	Phe
			100					105					110		
Ala	Val	Val	Leu	Tyr	Val	Lys	Lys	Phe	Ile	Pro	Glu	Glu	Ile	Ala	Val
			115					120					125		
Gln	Arg	Arg	His	Asp	Gly	Pro	Ser	Glu	Glu	Val	Asp	Arg	Arg	Thr	Ile
			130			135					140				
Val	Ala	Leu	Leu	Asn	Asp	Ser	Trp	Gln	Thr	Ser	Thr	Leu	Gly	Arg	Arg
145				150						155					160
Lys	Leu	Ile	Met	Gly	Leu	Ala	Gly	Gly	Gly	Ala	Val	Leu	Ala	Gly	Leu
				165					170					175	
Thr	Ile	Ile	Ala	Pro	Met	Gly	Gly	Met	Ile	Lys	Asn	Pro	Trp	Asn	Pro
			180					185						190	
Lys	Glu	Gly	Pro	Met	Asp	Val	Gln	Gly	Asp	Gly	Thr	Leu	Trp	Thr	Ser
			195				200						205		
Gly	Trp	Thr	Leu	Val	Glu	Asn	Asp	Val	Lys	Val	Tyr	Leu	Gly	Arg	Asp
			210			215					220				
Thr	Ala	Ala	Ile	Ala	Glu	Ser	His	Thr	Asp	Ala	Thr	Gly	Glu	His	Trp
225				230						235					240
Ser	Thr	Thr	Gly	Val	Ser	Arg	Leu	Val	Arg	Met	Arg	Pro	Glu	Asp	Leu
				245					250					255	
Ala	Ala	Ala	Ser	Met	Glu	Thr	Val	Phe	Pro	Leu	Pro	Ala	Glu	Met	Val
			260					265					270		
Asn	Asp	Gly	Ala	Glu	Tyr	Asp	Pro	Ala	Lys	Asp	Val	Tyr	Glu	His	Gln
		275					280					285			
Met	His	Ser	Val	His	Gly	Pro	Arg	Asn	Ala	Val	Met	Leu	Ile	Arg	Leu
			290			295					300				
Arg	Thr	Ala	Asp	Ala	Glu	Lys	Val	Ile	Glu	Arg	Glu	Gly	Gln	Glu	Ser
305				310						315					320
Phe	His	Tyr	Gly	Asp	Tyr	Tyr	Ala	Tyr	Ser	Lys	Ile	Cys	Thr	His	Ile
				325					330					335	
Gly	Cys	Pro	Thr	Ser	Leu	Tyr	Glu	Ala	Gln	Thr	Asn	Arg	Ile	Leu	Cys
			340					345					350		
Pro	Cys	His	Gln	Ser	Gln	Phe	Asp	Ala	Leu	His	Tyr	Gly	Lys	Pro	Val
			355				360					365			
Phe	Gly	Pro	Ala	Ala	Arg	Ala	Leu	Pro	Gln	Leu	Pro	Ile	Thr	Val	Asp
			370			375					380				

Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly
385 390 395 400

Pro Ala Phe Trp Glu Arg Lys Ser
405

<210> 667
<211> 1053
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1030)
<223> RXA02740

<400> 667
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tatgagtgat ttgaaaatgc aacgttctgg aggagaaccc ttg gac acg atc aag 115
Leu Asp Thr Ile Lys
1 5

gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163
Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
10 15 20

gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211
Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
25 30 35

gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259
Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
40 45 50

gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307
Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
55 60 65

gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355
Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
70 75 80 85

gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403
Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
90 95 100

ctg tgg ctg ctg tgc gat tgc atg ctc gcc ggc atc ttc gtg ttg atc 451
Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
105 110 115

acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499
Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
120 125 130

acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547
Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
135 140 145

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ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595
Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
150 155 160 165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643
Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
170 175 180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691
Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
185 190 195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739
Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln
200 205 210

gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787
Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr
215 220 225

ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835
Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val
230 235 240 245

att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883
Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly
250 255 260

atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931
Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser
265 270 275

aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979
Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val
280 285 290

ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027
Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly Trp Thr Thr Thr Phe
295 300 305

ttc taaaagcttg cttttcgacg aaa 1053
Phe
310

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<210> 668

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 668

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Leu Asp Thr Ile Lys Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile
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Glu Leu Leu Leu Val Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg
20 25 30

Gly Glu Asn Asn Ile Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp
35 40 45

Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp

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50 55 60
 Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His
 65 70 75 80
 Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val
 85 90 95
 Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly
 100 105 110
 Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys
 115 120 125
 Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala
 130 135 140
 Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe
 145 150 155 160
 Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met
 165 170 175
 Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys
 180 185 190
 Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val
 195 200 205
 Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala
 210 215 220
 Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr
 225 230 235 240
 Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile
 245 250 255
 Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys
 260 265 270
 Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu
 275 280 285
 Ser Val Asp Ala Val Leu Gly Leu Glu Thr Ile Gly Glu Met Leu Gly
 290 295 300
 Trp Thr Thr Thr Phe Phe
 305 310

<210> 669

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1138)

<223> RXA02743

<400> 669

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aattgtataa aactagccat gacctgctag gatcagcgac gtg tct act tca gat 115
 Val Ser Thr Ser Asp
 1 5

gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca 163
 Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala
 10 15 20

ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc 211
 Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe
 25 30 35

cag gga ggc atc acc gtt acg ggc tct atc gtc cgt gtc aca ggc tcc 259
 Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val Arg Val Thr Gly Ser
 40 45 50

ggc ctc ggt tgt gat acc tgg cca cta tgc cac gaa ggt tca cta gtc 307
 Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His Glu Gly Ser Leu Val
 55 60 65

cca gtc gca ggc gca gca cca tgg atc cac cag gca gtg gaa ttt ggt 355
 Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln Ala Val Glu Phe Gly
 70 75 80 85

aac cgc atg ctc act ttc gtg ctt gct gcc gca gcg ctt gcg ttg ttc 403
 Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala Ala Leu Ala Leu Phe
 90 95 100

att gca gtt ctt ggc gca aaa cgc cgc cgc gag atc ctg gtc cat tcc 451
 Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu Ile Leu Val His Ser
 105 110 115

ttc atc cag ggt ttg ggc atc atc ttg cag gct gtc atc ggt ggc atc 499
 Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala Val Ile Gly Gly Ile
 120 125 130

acc gtg ctg gtt gat ttg cac tgg tac gcc gtt gct ttg cac ttc ctg 547
 Thr Val Leu Val Asp Leu His Trp Tyr Ala Val Ala Leu His Phe Leu
 135 140 145

cca tcc atg atc ctt gtt ttc atg gcc gcg att ttg tac acc cgc atc 595
 Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile Leu Tyr Thr Arg Ile
 150 155 160 165

ggc gag ccc gat gac ggc gag att acc acc aca ttc ccc acg tgg atc 643
 Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr Phe Pro Thr Trp Ile
 170 175 180

cgc aat gta gct gtc att ggt gca gta gcg ctc tcc gta gta ctg atc 691
 Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu Ser Val Val Leu Ile
 185 190 195

acc ggc acc atg acc acc ggc gct ggc gtt cac tct ggc gat gca tca 739
 Thr Gly Thr Met Thr Thr Gly Ala Gly Val His Ser Gly Asp Ala Ser
 200 205 210

atc acc atg gat gat cgc ctc gat gtc agc atc gac ttg atg gcc cac 787
 Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile Asp Leu Met Ala His

215	220	225	
atc cac ggc tac agc atg	tac atc tac ctc ttc ttc acc ctc atc gtg		835
Ile His Gly Tyr Ser Met	Tyr Ile Tyr Leu Phe Phe Thr Leu Ile Val		
230	235	240	245
gtc gcc ggt ctg tac aag	gca aaa acc acc aag cac aac aag cag ctt		883
Val Ala Gly Leu Tyr Lys	Ala Lys Thr Thr Lys His Asn Lys Gln Leu		
	250	255	260
ggc ctc atg ctg att ctg	ttc att ctg att cag gca ggt atc ggc atc		931
Gly Leu Met Leu Ile Leu	Phe Ile Leu Ile Gln Ala Gly Ile Gly Ile		
	265	270	275
ttg cag tac cgc atg ggt	gtg cca cgc tgg agc atc cca ttc cac atc		979
Leu Gln Tyr Arg Met Gly	Val Pro Arg Trp Ser Ile Pro Phe His Ile		
	280	285	290
gca atg tct tct gtc gtt	gtt gcc ttc act tcc ctt ctg tgg gcg cag		1027
Ala Met Ser Ser Val Val	Val Ala Phe Thr Ser Leu Leu Trp Ala Gln		
	295	300	305
ggc cgt ata cgc gtc ggc	ggc aaa gcc acc gtt act ggt tct gtt gat		1075
Gly Arg Ile Arg Val Gly	Gly Lys Ala Thr Val Thr Gly Ser Val Asp		
	310	315	320
ggc gat att aag aac gag	atc att acg aac ccc ttt gag aag aaa tca		1123
Gly Asp Ile Lys Asn Glu	Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser		
	330	335	340
aag cag cct gtt aaa	taacacgcaa ctgtatcggt aaa		1161
Lys Gln Pro Val Lys			
	345		

<210> 670

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

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Leu Leu Leu Ile Phe Gln Gly Gly Ile Thr Val Thr Gly Ser Ile Val	
35 40 45	
Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His	
50 55 60	
Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln	
65 70 75 80	
Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala	
85 90 95	
Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu	
100 105 110	

Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
 115 120 125
 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val
 130 135 140
 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile
 145 150 155 160
 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr
 165 170 175
 Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu
 180 185 190
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His
 195 200 205
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile
 210 215 220
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe
 225 230 235 240
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys
 245 250 255
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln
 260 265 270
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser
 275 280 285
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser
 290 295 300
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val
 305 310 315 320
 Thr Gly Ser Val Asp Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro
 325 330 335
 Phe Glu Lys Lys Ser Lys Gln Pro Val Lys
 340 345

<210> 671

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA01227

<400> 671

ggataatcga aaatatgtgc cccttggtga agggtcgggg agctaataagg atgacagtga 60
 acctattttc cacgtcttta tccgtagtat tggagatccg atg acc tac aca atc 115

	Met	Thr	Tyr	Thr	Ile	
	1				5	
gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt						163
Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys						
ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc						211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro						
gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa						259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu						
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc						307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr						
ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tgc cca ggc ggt gcc						355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala						
gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg						403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu						
ccg cca cag aac cag aac taggacctga taccggccct aaa						444
Pro Pro Gln Asn Gln Asn						

<210> 672

<211> 107

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala																			
1				5				10											15
Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met																			
				20				25											30
Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro																			
				35				40											45
Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu																			
				50				55											60
Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly																			
				65				70											80
Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln																			
				85				90											95
Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn																			
				100															105

<210> 673


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<220>  
<221> CDS  
<222> (101)..(415)  
<223> RXA01865
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<210> 674
<211> 105
<212> PRT
<213> Corynebacterium glutamicum
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<400> 674
Met Thr Tyr Thr Ile Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala
  1             5             10             15
Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
          20             25             30
Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
      35             40             45
Ala Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu

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50 55 60

Trp Leu Asp Tyr Asn Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
65 70 75 80

Ser Pro Gly Gly Ala Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro
85 90 95

Met Ile Ala Ala Leu Pro Pro Gln Ala
100 105

<210> 675
<211> 441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> RXA00680

<400> 675
ttcttgcattc cccagaagcc gaatacatca ctgggcaaac actcatcggt gatgggtggcc 60

gacagttcat ctaagtacta aaagttctaa ggagaagatc atg tct act att cat 115
Met Ser Thr Ile His
1 5

ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt 163
Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly
10 15 20

gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt 211
Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val
25 30 35

gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt 259
Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val
40 45 50

gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat 307
Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp
55 60 65

gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg 355
Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu
70 75 80 85

tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg 403
Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr
90 95 100

cca gaa acg caa gtg tgaggttgaa tcatgaatac ttc 441
Pro Glu Thr Gln Val
105

<210> 676
<211> 106
<212> PRT

<213> Corynebacterium glutamicum

<400> 676

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Met Ser Thr Ile His Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile
 1             5             10             15

Glu Ala Thr Val Gly Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly
      20             25             30

Val Pro Gly Ile Val Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr
      35             40             45

Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met
      50             55             60

Glu Glu Met Glu Asp Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu
      65             70             75             80

Asp Cys Ser Arg Leu Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp
      85             90             95

Leu Ser Leu Thr Thr Pro Glu Thr Gln Val
      100             105

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<210> 677

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1366)

<223> RXA00679

<400> 677

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ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct 115
                                   Met Asn Thr Ser Ala
                                   1             5

gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu
      10             15             20

gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu
      25             30             35

ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu
      40             45             50

ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn
      55             60             65

gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc 355
Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile
      70             75             80             85

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gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc	403
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala	
90 95 100	
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc	451
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg	
105 110 115	
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac	499
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr	
120 125 130	
ctg cgc aac gcg gac gac gcc ttg gcg ctc aaa gcg atg att ggt tct	547
Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys Ala Met Ile Gly Ser	
135 140 145	
gtc acc gat gcc gtt gta gtc ggt ggt ggg ttc atc gga ttg gaa gct	595
Val Thr Asp Ala Val Val Val Gly Gly Gly Phe Ile Gly Leu Glu Ala	
150 155 160 165	
gcg tgt tcg ctt cat gac ctc ggc aaa aat gtc acc gtc ctg gaa tat	643
Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val Thr Val Leu Glu Tyr	
170 175 180	
ggt ccg cgt ctg att ggc cga gcg gtg ggt gaa gaa acc gca gca ttc	691
Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu Glu Thr Ala Ala Phe	
185 190 195	
ttc ctc gaa caa cac cgt tcc cgt ggc gta aat atc gtg ctt gat gcc	739
Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn Ile Val Leu Asp Ala	
200 205 210	
cgc atg aaa cag ttt gtg ggc aag gat gga aag ctc agc ggc att gag	787
Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys Leu Ser Gly Ile Glu	
215 220 225	
cta gaa gat ggc aca gta att cct gcc caa cta gtc att gtg ggc atc	835
Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu Val Ile Val Gly Ile	
230 235 240 245	
ggt gtc att ccg aac aca gaa ctt gcc gct gtt ctg ggc tta gac atc	883
Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val Leu Gly Leu Asp Ile	
250 255 260	
aac aac ggc atc gtg gtg gat aaa cat gcc gtc gcg tca gat ggc acc	931
Asn Asn Gly Ile Val Val Asp Lys His Ala Val Ala Ser Asp Gly Thr	
265 270 275	
acc att gcg att ggc gat gtc gcc aac att ccc aat cca atc cct ggt	979
Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro Asn Pro Ile Pro Gly	
280 285 290	
tcc ccc gct gat gaa cgc atc cga cta gaa agc gtc aat aac gcc atc	1027
Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser Val Asn Asn Ala Ile	
295 300 305	
gag cac gca aag atc gct gca tac tca ctc gtc ggc cag ccc gaa gcc	1075
Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val Gly Gln Pro Glu Ala	
310 315 320 325	

tac gcc gga atc ccc tgg ttc tgg tcc aac caa ggc gat ctc aaa cta 1123
 Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln Gly Asp Leu Lys Leu
 330 335 340

caa att gca gga ctt acc ctt ggt tat gac agc aca gta atc cga cag 1171
 Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser Thr Val Ile Arg Gln
 345 350 355

gat ccc gag aaa aag aag ttc tct gtc ctt tat tac cgt ggc gac aac 1219
 Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr Tyr Arg Gly Asp Asn
 360 365 370

atc atc gcc gcc gat tgt gtc aac gct cca ctg gat ttc atg gct gtg 1267
 Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val
 375 380 385

cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala
 390 395 400 405

gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr
 410 415 420

cga tgactcgacg taatttaccc gct 1389
 Arg

<210> 678

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Asn Thr Ser Ala Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln
 1 5 10 15

Ser Gly Val Gln Leu Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu
 20 25 30

Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro
 35 40 45

Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu
 50 55 60

Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val
 65 70 75 80

Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly
 85 90 95

Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu
 100 105 110

Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu
 115 120 125

Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys
 130 135 140

Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
 145 150 155 160
 Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
 165 170 175
 Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
 180 185 190
 Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
 195 200 205
 Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
 210 215 220
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
 225 230 235 240
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
 245 250 255
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
 260 265 270
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
 275 280 285
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
 290 295 300
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
 305 310 315 320
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
 325 330 335
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
 340 345 350
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
 355 360 365
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
 370 375 380
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
 385 390 395 400
 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
 405 410 415
 Asp Leu Glu Val Thr Arg
 420

<210> 679

<211> 1074

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA00224

<400> 679

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acctcatcta gccactatct tcacaaagga gaacatttaa atg tct att tct tat 115
                               Met Ser Ile Ser Tyr
                               1 5

gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163
Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu Pro Val Thr Leu Glu
          10          15          20

ttg atc act gct gct cgc gca ctc ggt gac gtc gtt gcc gtt gtc gtt 211
Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val Val Ala Val Val Val
          25          30          35

ggc gag cca ggt gcc ggc gta aac ctt gct gct gag ctc ggc aat tgg 259
Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala Glu Leu Gly Asn Trp
          40          45          50

ggt gca gca cag gtt gtt tcc gct gaa atc tct ggc gct tcc aac cgt 307
Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser Gly Ala Ser Asn Arg
          55          60          65

ttg atc ttg cct gct gtt gat gcg ctg cac att ttg gct gcg aac aac 355
Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile Leu Ala Ala Asn Asn
          70          75          80          85

cca ggt cca att gtt atc gct gca act gca agc ggt aat gag atc gct 403
Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser Gly Asn Glu Ile Ala
          90          95          100

ggt cgt ttg gct gcc cgt ttg gct tct ggt gtg ctc acc gat gtc gtc 451
Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val Leu Thr Asp Val Val
          105          110          115

gga atc aat gcc gac cgc acc gca cag cag tcc att ttc ggc gac acc 499
Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser Ile Phe Gly Asp Thr
          120          125          130

att cag gtg tcc gct gca gtt ggt ggc gct tca ccg ctg tac acc ctg 547
Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser Pro Leu Tyr Thr Leu
          135          140          145

cgt cca ggt gcc ctt gat ggc gtg gcc gtt cct gca acc ggt gaa ttg 595
Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro Ala Thr Gly Glu Leu
          150          155          160          165

gca acc att gag atc cca ggc gca acc gcc aag gat gtc acc atc acc 643
Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys Asp Val Thr Ile Thr
          170          175          180

tcc ttc acg cca agc acc cag agc gat cgc cct gag ctg cca cag gca 691
Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro Glu Leu Pro Gln Ala
          185          190          195

aag gtc gtt atc gca ggt gga cgt ggt gtc gga agc gaa gaa aac ttc 739

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Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly Ser Glu Glu Asn Phe
 200 205 210
 cgc agc atc gtt gaa cca ctg gca gat gca ttg ggc ggt gcc gtt ggc 787
 Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu Gly Gly Ala Val Gly
 215 220 225
 gca acc cgc gac gcc gtt gat ctg ggc tac tac cca ggc gag tac cag 835
 Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr Pro Gly Glu Tyr Gln
 230 235 240 245
 gtt ggt cag acc ggt gtc acc gtg tcc cca gac ctc tac atc ggc ctc 883
 Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp Leu Tyr Ile Gly Leu
 250 255 260
 ggc att tcc ggt gca att cag cac act tct ggt atg cag acc gca aag 931
 Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly Met Gln Thr Ala Lys
 265 270 275
 aag gtt att gtg atc aac aac gat gag gac gcg ccg atc ttc cag att 979
 Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala Pro Ile Phe Gln Ile
 280 285 290
 gcg gac ctc ggt gtc gtt ggc gac ctc ttt gac atc gcc cct gcg ctc 1027
 Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp Ile Ala Pro Ala Leu
 295 300 305
 atc gaa gag atc aac aag cgc aag taggagtttt gaacactttt tat 1074
 Ile Glu Glu Ile Asn Lys Arg Lys
 310 315

<210> 680

<211> 317

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

Met Ser Ile Ser Tyr Val Leu Val Glu Gln Leu Asp Gly Arg Pro Glu
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 Pro Val Thr Leu Glu Leu Ile Thr Ala Ala Arg Ala Leu Gly Asp Val
 20 25 30
 Val Ala Val Val Val Gly Glu Pro Gly Ala Gly Val Asn Leu Ala Ala
 35 40 45
 Glu Leu Gly Asn Trp Gly Ala Ala Gln Val Val Ser Ala Glu Ile Ser
 50 55 60
 Gly Ala Ser Asn Arg Leu Ile Leu Pro Ala Val Asp Ala Leu His Ile
 65 70 75 80
 Leu Ala Ala Asn Asn Pro Gly Pro Ile Val Ile Ala Ala Thr Ala Ser
 85 90 95
 Gly Asn Glu Ile Ala Gly Arg Leu Ala Ala Arg Leu Ala Ser Gly Val
 100 105 110
 Leu Thr Asp Val Val Gly Ile Asn Ala Asp Arg Thr Ala Gln Gln Ser
 115 120 125

Ile Phe Gly Asp Thr Ile Gln Val Ser Ala Ala Val Gly Gly Ala Ser
 130 135 140
 Pro Leu Tyr Thr Leu Arg Pro Gly Ala Leu Asp Gly Val Ala Val Pro
 145 150 155 160
 Ala Thr Gly Glu Leu Ala Thr Ile Glu Ile Pro Gly Ala Thr Ala Lys
 165 170 175
 Asp Val Thr Ile Thr Ser Phe Thr Pro Ser Thr Gln Ser Asp Arg Pro
 180 185 190
 Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
 195 200 205
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
 210 215 220
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
 225 230 235 240
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
 245 250 255
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
 260 265 270
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
 275 280 285
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
 290 295 300
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
 305 310 315

<210> 681
 <211> 909
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(886)
 <223> RXA00225

<400> 681
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 Met Ser Thr Ile Val
 1 5
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu
 10 15 20
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu

25	30	35	
atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 40 45 50			259
ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 55 60 65			307
ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 70 75 80 85			355
atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr 90 95 100			403
gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu 105 110 115			451
atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro 120 125 130			499
ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser 135 140 145			547
gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn 150 155 160 165			595
cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile 170 175 180			643
tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met 185 190 195			691
gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly 200 205 210			739
gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr 215 220 225			787
gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala 230 235 240 245			835
tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu 250 255 260			883
atc tagccactat cttcacaag gag Ile			909

<210> 682

<211> 262

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 682

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Met Ser Thr Ile Val Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser
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Lys Arg Thr Leu Glu Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp
          20           25           30

Arg Val Leu Asp Glu Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg
      35           40           45

Leu Arg Glu Ser Asn Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser
      50           55           60

Ala Gly Pro Ala Gly Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met
      65           70           75           80

Gly Ala Asp Glu Ala Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser
          85           90           95

Asp Leu Leu Gly Thr Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile
      100          105          110

Ala Gly Val Ala Leu Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser
      115          120          125

Met Gly Ala Leu Pro Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala
      130          135          140

Leu Thr Asn Leu Ser Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala
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Thr Arg Ile Asp Asn His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro
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Ala Val Val Ser Ile Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn
          180          185          190

Phe Lys Gly Ile Met Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser
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Leu Ala Glu Ile Gly Val Ala Pro Glu Gln Val Gly Leu Ser His Ala
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Ala Thr Ala Val Thr Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly
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Leu	Pro	Glu	Ala	Met	Ala	Ala	Ala	Thr	Pro	Val	Ser	Ala	Phe	Leu	His	
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Pro	Arg	Asp	Met	Ser	His	Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu		
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 700 705 710

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 Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro
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 acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319
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 Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
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 Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
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 Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
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 Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
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 Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
 115 120 125

 His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
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 His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
 145 150 155 160

 Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met

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His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser				
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 515 520 525
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 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro
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 Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
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 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
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 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
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 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
 610 615 620
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
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 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
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 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
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 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
 675 680 685
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
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 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
 705 710 715 720
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<212> DNA

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Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Leu Val Gly Ala
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Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp
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His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala
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Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu
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Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu
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gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat 643
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Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met	
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Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln Phe Leu Val Glu	
265 270 275	
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Gly Leu Val Val Val Ile Ile Met Met Val Val Arg His Gln Pro Ala	
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Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser Thr Val Leu Val	
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Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val Trp Gly Leu Leu	
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Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly	
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Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr Ile Leu Val Glu	
345 350 355	
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Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val Leu Gly Met Ala	
360 365 370	
gct gtc gtc atc ggt gcg atg gtg gct tcc atg cct cgt cat ccg ttt	1267
Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro Arg His Pro Phe	
375 380 385	
gcc aag ggc acc cac cct cgc ccc ttt ggc caa tca cag ttg aac tcc	1315
Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser	
390 395 400 405	
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Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro Ala Leu Cys Phe	
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Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp Pro Gly Gly Gly	
425 430 435	
ttc atc gca gcc cta att gcc ggt ggc gcg ctg atg ctc ctg tac ctg	1459
Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu	
440 445 450	
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Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn Val Pro Phe Ile
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ctc act ggt gcg ggc atc ttg atg gca gtg ttc tcg ggc gta ctg gga 1555
 Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser Gly Val Leu Gly
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 Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe Asn Phe Val Gly
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cag cac tgg acc acc tcg atg atc ttc gac ctc ggc gtg tac ctg gcc 1651
 Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly Val Tyr Leu Ala
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gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg 1699
 Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu
 520 525 530

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 Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly
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 Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu
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 35 40 45

Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
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His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
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Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
 85 90 95

Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met

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Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu
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Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly
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Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr
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Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg
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Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala
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Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp
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Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn
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Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser
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Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met
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Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val
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Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn
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Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu
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 Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro
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 Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe
 465 470 475 480
 Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His
 485 490 495
 Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu
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 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly
 515 520 525
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 530 535 540
 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu
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 Asn Lys Glu Glu Ala Asn Arg
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 Met Ala Met Asp Val
 1 5
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 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
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 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
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 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
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Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val	
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Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr	
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acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt	403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly	
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gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg	451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr	
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Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val	
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Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr	
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Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn	
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Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly	
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Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly	
185 190 195	
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Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala	
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Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr	
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Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr	
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Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn	
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Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser	
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Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg	
280 285 290	
gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg	1027

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Met	Ala	Phe	Thr	Ser	Asp	Asp	Pro	Gln	Arg	Ala	Leu	Ala	Ala	Gly	Leu		
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Leu	Tyr	Thr	Leu	His	His	Met	Ile	Thr	Ile	Ala	Ala	Leu	Val	Leu	Thr		
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tcc	ggc	gca	atc	gaa	gaa	acc	tac	ggc	acc	gg	atg	ttg	tcc	aag	ctg	1171	
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Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala		
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Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly		
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Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala		
390						395				400					405		
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363	
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu		
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Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala		
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cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507	
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala		
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Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn		
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acc	gat	gca	tac	caa	cag	gct	gtg	ctc	gg	gaa	aat	gcc	atc	gga	gtg	1603	
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val		
				490					495					500			
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650	
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<213> Corynebacterium glutamicum

<400> 688

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 Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
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 Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
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 Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
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 Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
 85 90 95
 Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
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 115 120 125
 Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130 135 140
 Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145 150 155 160
 Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
 165 170 175
 Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
 180 185 190
 Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
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 Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
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 Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
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 Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp
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 Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala
 260 265 270
 Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu
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Ala	Val	Phe	Ala	Ala	Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe		
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Gly	Gly	Ala	Met	His	Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser		
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Pro	Ala	Lys	Ile	Ala	Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly		
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                                     Met Ala Met Asp Val
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Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
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Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu	Phe	Ala	His	Thr	Ala		
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Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu	Tyr	Val	Gly	Gly	Val		
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Ala	Ile	Pro	Phe	Ala	Ala	Asp	Thr	Phe	Ser	Ala	Ile	Met	Leu	Ile	Thr		
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Thr	Ser	Ile	Val	Ala	Val	Ala	Ala	Asn	Trp	Phe	Ala	Thr	Ile	Val	Gly		
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Glu	Thr	Arg	Ala	Arg	Phe	Tyr	Pro	Ala	Leu	Thr	Leu	Met	Leu	Ile	Thr		
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Gly	Val	Asn	Gly	Ala	Leu	Leu	Thr	Ala	Asp	Leu	Phe	Asn	Phe	Phe	Val		
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ttc	atc	gaa	gtg	atg	ctg	ctg	cct	tcc	tat	ggt	ttg	atc	gcc	atg	acc	547	
Phe	Ile	Glu	Val	Met	Leu	Leu	Pro	Ser	Tyr	Gly	Leu	Ile	Ala	Met	Thr		
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gga	acg	tgg	gcg	cgc	cta	gcc	tct	gga	cga	atc	ttc	gta	cta	gtc	aat	595	
Gly	Thr	Trp	Ala	Arg	Leu	Ala	Ser	Gly	Arg	Ile	Phe	Val	Leu	Val	Asn		
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Leu	Ser	Ala	Ser	Thr	Leu	Leu	Val	Ala	Gly	Val	Gly	Ile	Val	Tyr	Gly		
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Val	Ile	Gly	Ser	Val	Asn	Ile	Ala	Ala	Leu	Gln	Asp	Val	Val	Glu	Gly		
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Asn	Pro	Leu	Val	Ala	Ser	Ala	Met	Gly	Ile	Val	Val	Ile	Ala	Ile	Ala		
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Val	Lys	Ala	Gly	Val	Phe	Pro	Val	His	Thr	Trp	Leu	Pro	Arg	Thr	Tyr		
	215					220					225						
cct	ggt	aca	tca	gca	gct	gtg	atg	ggg	ttg	ttc	tcc	ggt	ttg	cac	acc	835	
Pro	Gly	Thr	Ser	Ala	Ala	Val	Met	Gly	Leu	Phe	Ser	Gly	Leu	His	Thr		
230					235					240					245		
aaa	gtc	gcg	gta	tac	atg	ctc	tat	cgc	att							865	
Lys	Val	Ala	Val	Tyr	Met	Leu	Tyr	Arg	Ile								
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<211> 255

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 690

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Ala Ser Ala Ile Ala Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile
          20              25              30

Leu His Ile Ile Val Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu
      35              40              45

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50              55              60

Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65              70              75              80

Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
          85              90              95

Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
          100              105              110

Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115              120              125

Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130              135              140

Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145              150              155              160

Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
          165              170              175

Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
          180              185              190

Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
 195              200              205

Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210              215              220

Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
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Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
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<211> 2118

<212> DNA

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<220>

<221> CDS

<222> (1)..(2118)

<223> RXA00913

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ctt gca ctg acc gtt gcg cac tcc ttg ttt aag gca aca ttg ttc atg 96
Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
             20             25             30

aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa 144
Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
             35             40             45

ctc tcc ggt ctg tgg cgt aaa caa ccg atc ctg ttc gcc gtt gct gct 192
Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
             50             55             60

gtt tcg gcg gcg tcc atg gct ggt att ccg cca ctg ttt ggt ttt atc 240
Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
             65             70             75             80

gcc aag gaa aca gcg ctg gat acc gtg ttg aat gag cag atg ttg cat 288
Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
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ggc atg cca ggt cga ttg atg ctg gct ggc atc gtt ttg ggt tcc atc 336
Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
             100             105             110

ttc acc atg gca tat tcc tgc tac ttc ctg tac gaa gcc ttt gcc acg 384
Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
             115             120             125

aag cac tcc aaa ttc cca gag gcc aac ggt gtc tca cct gca gtg gag 432
Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
             130             135             140

gca atg cat ccg gtg aag ttt aag ctg tgg atc gca cct gtc atc ctg 480
Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
             145             150             155             160

gct att ttg acc gta gtg ttt ggt gtt ttc ccc aag cca gtg tcg gaa 528
Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
             165             170             175

gca att gtc acg cat ctt gat aac gtc acg cca tcg ctt gat gat gtc 576
Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
             180             185             190

cac acc aaa ctg gcc ttg tgg cat ggt ctg aat cta ccg ctg ctg ctg 624
His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
             195             200             205

tct gtg gtg atc atc att tcc gga ttc atc atc ttc tgg gag cga gac 672
Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
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acc gtc gaa cgt ttg cgc cct aac acc gca gcg ttt ggc agt gcc gat 720

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Thr 225	Val	Glu	Arg	Leu	Arg 230	Pro	Asn	Thr	Ala	Ala 235	Phe	Gly	Ser	Ala	Asp 240	
acc Thr	gcc Ala	tac Tyr	gac Asp	gcc Ala 245	att Ile	ctt Leu	gat Asp	gca Ala	ctg Leu 250	cgt Arg	gtg Val	ctc Leu	tcc Ser	cac His 255	cgc Arg	768
ctg Leu	act Thr	gca Ala	tcc Ser 260	acc Thr	cag Gln	cgt Arg	ggt Gly	tct Ser 265	ttg Leu	acc Thr	ctg Leu	aac Asn 270	gtc Val	ggt Gly	gtg Val	816
atc Ile	ttc Phe	ttc Phe 275	gtc Val	ctc Leu	acg Thr	att Ile	ggt Val 280	ccg Pro	ctg Leu	atc Ile	gct Ala	ttg Leu 285	atc Ile	act Thr	ggc Gly	864
gaa Glu	caa Gln 290	agc Ser	gat Asp	gtc Val	cgc Arg	atg Met 295	gag Glu	ctg Leu	tgg Trp	gat Asp 300	agc Ser	cct Pro	att Ile	cag Gln	ggc Gly	912
ttc Phe 305	atc Ile	gcg Ala	gcc Ala	atc Ile	att Ile 310	atc Ile	gtc Val	ggt Val	gcg Ala	att Ile 315	gtg Val	gca Ala	acc Thr	acc Thr	atg Met 320	960
gat Asp	aac Asn	cgt Arg	ttg Leu	tct Ser 325	gcg Ala	ctg Leu	att Ile	ttg Leu 330	gtg Val	ggt Gly	gtg Val	aca Thr	ggt Gly	tat Tyr 335	ggc Gly	1008
att Ile	gcc Ala	ggt Val	atc Ile 340	ttc Phe	gcg Ala	cta Leu	cat His	ggc Gly 345	gca Ala	ccg Pro	gac Asp	ttg Leu 350	gcg Ala	cta Leu	acc Thr	1056
cag Gln	gtg Val	ctg Leu 355	gtg Val	gag Glu	acc Thr	atc Ile	gtc Val 360	atg Met	gtg Val	gta Val	ttc Phe 365	atg Met	ctg Leu	gtg Val	ctg Leu	1104
cgt Arg	aaa Lys 370	atg Met	ccg Pro	aca Thr	gaa Glu	gtt Val 375	gcg Ala	tgg Trp	aag Lys	gca Ala	gaa Glu 380	cct Pro	aaa Lys	cag Gln	tct Ser	1152
cgc Arg 385	gtg Val	cga Arg	gcg Ala	tgg Trp	ctt Leu 390	gct Ala	ggc Gly	gcc Ala	acc Thr	gga Gly 395	ttg Leu	tcc Ser	gtt Val	gtt Val	att Ile 400	1200
gtc Val	acc Thr	att Ile	ttt Phe	gcc Ala 405	atg Met	aat Asn	gct Ala	cgc Arg 410	acc Thr	act Thr	gaa Glu	ccg Pro	atc Ile	tct Ser 415	gta Val	1248
tac Tyr	atg Met	cag Gln	gat Asp 420	ctg Leu	gcc Ala	tat Tyr	gag Glu	atc Ile 425	gga Gly	cat His	ggc Gly	gca Ala	aac Asn 430	acc Thr	gtc Val	1296
aac Asn	gta Val 435	ctg Leu	ctc Leu	gta Val	gac Asp	ctg Leu	cgt Arg 440	ggt Gly	ttt Phe	gat Asp	acc Thr 445	ttc Phe	ggt Gly	gaa Glu	att Ile	1344
tcc Ser 450	gtc Val	ctt Leu	gtg Val	atc Ile	gcg Ala	gca Ala 455	acc Thr	ggt Gly	atc Ile	gcc Ala 460	tcc Ser	ctg Leu	gtc Val	tac Tyr	cga Arg	1392
aac Asn	cgc Arg	agc Ser	ttc Phe	cgc Arg	aag Lys	gat Asp	tct Ser	cgc Arg	aga Arg	cca Pro	acc Thr	ctg Leu	gct Ala	acc Thr	act Thr	1440

465	470	475	480	
ggt cgc cgt tgg ttg gct gct gct gtt gat acc gaa agg gcg cag aac				1488
Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn				
	485	490	495	
cgc tcg ctg atg gtt gat gtg gca acg cgc atc ctc ttc cct gcc atg				1536
Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met				
	500	505	510	
atc atg ttg tct gtg tac ttc ttc ttc gcc gga cac aac gcg ccg ggc				1584
Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly				
	515	520	525	
ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc				1632
Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg				
	530	535	540	
tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac				1680
Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp				
	545	550	555	560
gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg				1728
Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val				
	565	570	575	
ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att				1776
Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile				
	580	585	590	
tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg				1824
Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala				
	595	600	605	
ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg				1872
Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met				
	610	615	620	
cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg				1920
His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met				
	625	630	635	640
cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag				1968
Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln				
	645	650	655	
cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg				2016
Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser				
	660	665	670	
aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg				2064
Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser				
	675	680	685	
gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta				2112
Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu				
	690	695	700	
aag cag				2118
Lys Gln				
705				

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 <213> Corynebacterium glutamicum

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 20 25 30
 Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
 35 40 45
 Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
 50 55 60
 Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
 65 70 75 80
 Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
 85 90 95
 Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
 100 105 110
 Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
 115 120 125
 Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
 130 135 140
 Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
 145 150 155 160
 Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
 165 170 175
 Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
 180 185 190
 His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
 195 200 205
 Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
 210 215 220
 Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
 225 230 235 240
 Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
 245 250 255
 Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
 260 265 270
 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
 275 280 285

Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
 290 295 300
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
 305 310 315 320
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
 325 330 335
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
 340 345 350
 Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
 355 360 365
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
 370 375 380
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
 385 390 395 400
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
 405 410 415
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
 420 425 430
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
 435 440 445
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
 450 455 460
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
 465 470 475 480
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
 485 490 495
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
 500 505 510
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
 515 520 525
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
 530 535 540
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
 545 550 555 560
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
 565 570 575
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
 580 585 590
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
 595 600 605

Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
 610 615 620
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
 625 630 635 640
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
 645 650 655
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
 660 665 670
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
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 Lys Gln
 705

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 <212> DNA
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 <223> RXA00909

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 Val Leu Ile Leu Phe
 1 5
 ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163
 Leu Ala Leu Thr Ala Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
 10 15 20
 ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211
 Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
 25 30 35
 ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259
 Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
 40 45 50
 ggt gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307
 Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
 55 60 65
 atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355
 Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
 70 75 80 85
 tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403
 Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp

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Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe				
	105	110	115	
gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg				499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met				
	120	125	130	
tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt				547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly				
	135	140	145	
tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg				595
Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu				
	150	155	160	165
atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg				643
Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu				
	170	175	180	
atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac				691
Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr				
	185	190	195	
tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt				739
Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Ala Leu				
	200	205	210	
atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc				787
Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe				
	215	220	225	
tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg				835
Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu				
	230	235	240	245
cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc				883
His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu				
	250	255	260	
tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg				931
Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro				
	265	270	275	
ttg ggc atg ttg acc atg ctc atg				955
Leu Gly Met Leu Thr Met Leu Met				
	280	285		

<210> 694

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 694

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20				25				30							
Val	Pro	Gly	Ile	Gly	Phe	Phe	Trp	Val	Leu	Ser	Glu	Phe	Ile	Lys	Gly
		35					40						45		
Thr	Phe	Lys	Asp	Gly	Gly	Glu	Leu	Leu	Leu	His	Tyr	Ala	Trp	Met	Pro
	50					55					60				
Ser	Ala	His	Leu	Asn	Ile	Asp	Phe	Arg	Met	Asp	Ser	Leu	Ala	Ala	Leu
	65				70					75					80
Phe	Ser	Leu	Ile	Val	Leu	Gly	Val	Gly	Ala	Leu	Val	Leu	Leu	Tyr	Cys
				85					90					95	
Trp	Gly	Tyr	Phe	Asp	Ser	Asn	Ala	Gly	Arg	Leu	Ser	Ala	Phe	Gly	Ala
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Glu	Leu	Val	Ala	Phe	Ala	Met	Ala	Met	Phe	Gly	Leu	Val	Ile	Ser	Asp
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Asn	Ile	Leu	Leu	Met	Tyr	Val	Phe	Trp	Glu	Ile	Thr	Ser	Val	Leu	Ser
	130					135					140				
Phe	Leu	Leu	Val	Gly	Tyr	Tyr	Gly	Glu	Arg	Ala	Ser	Ser	Arg	Arg	Ser
	145				150					155					160
Ala	Gly	Gln	Ala	Leu	Met	Val	Thr	Thr	Leu	Gly	Gly	Leu	Ala	Met	Leu
				165					170					175	
Val	Gly	Ile	Ile	Leu	Met	Gly	Thr	Gln	Thr	Gly	Val	Trp	Arg	Phe	Ser
			180					185					190		
Glu	Ile	Pro	Ala	Tyr	Ser	Ser	Ser	Trp	Ala	Asp	Val	Pro	Tyr	Ile	Ser
		195					200					205			
Ala	Ala	Ala	Ala	Leu	Ile	Leu	Ala	Gly	Ala	Leu	Ser	Lys	Ser	Ala	Ile
		210				215					220				
Ala	Pro	Thr	His	Phe	Trp	Leu	Pro	Gly	Ala	Met	Ala	Ala	Pro	Thr	Pro
					230					235					240
Val	Ser	Ala	Tyr	Leu	His	Ser	Ala	Ala	Met	Val	Lys	Ala	Gly	Ile	Tyr
				245					250					255	
Leu	Val	Ala	Arg	Leu	Ser	Pro	Asp	Leu	Asn	Val	Val	Gly	Ser	Trp	Tyr
			260					265					270		
Leu	Ile	Ile	Ile	Pro	Leu	Gly	Met	Leu	Thr	Met	Leu	Met			
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<223> RXA00700
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 Met Ile Asn Ala Ile
 1 5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
 Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
 10 15 20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
 Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe
 25 30 35

ctg tcc gac aaa gcc caa gcg ccc ctc tac atc gcg atc gtc att ccc 259
 Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile Ala Ile Val Ile Pro
 40 45 50

ctc gtg ctg gcc gct gtc atc gcc gaa atc agt gaa aac gga ttc gac 307
 Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser Glu Asn Gly Phe Asp
 55 60 65

gtt aaa gcc gta gcc atg ctc ggc gtc ctc acc gcc atg gtt gcc gta 355
 Val Lys Ala Val Ala Met Leu Gly Val Leu Thr Ala Met Val Ala Val
 70 75 80 85

gtc cga cca ttc ggt gcc ggc gca gca ggc ttt gaa gca gtc ttc ttt 403
 Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe Glu Ala Val Phe Phe
 90 95 100

gtc ctc atc ctc ggc gga cga gcc ttc gga ccc ggc ttc gga ttc atc 451
 Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro Gly Phe Gly Phe Ile
 105 110 115

ctc ggc aac acc gga ctg ttc gca tcc gcg ctg ctc acc gca gga atc 499
 Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu Leu Thr Ala Gly Ile
 120 125 130

gga ccg tgg ctc ccc tac caa atg ctc gca gcc gcc tgg gtc agc ttc 547
 Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala Ala Trp Val Ser Phe
 135 140 145

ggc gcc ggc cta ctc ccc caa gta cgc ggc aaa aag gaa atg ctc atc 595
 Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys Lys Glu Met Leu Ile
 150 155 160 165

atc gtc cta tac gcc atc gtc tct tca ctc ggc tac gga acc atg atg 643
 Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly Tyr Gly Thr Met Met
 170 175 180

aac atg agc ttc tgg ccc tac gcc atc ggt gtc acc agc ggg ctt tcc 691
 Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val Thr Ser Gly Leu Ser
 185 190 195

ttc aca ccc ggc gcg ccc gtc ctg gaa aac ctc cac acc ttc atg ctg 739
 Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu His Thr Phe Met Leu
 200 205 210

ttc tgc ctc acc aca tcc atg ggt tgg gat ctc ggc cgc gcc ttc ttc 787
 Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu Gly Arg Ala Phe Phe

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215                220                225
acc tca gtg cta tta ctg ctc aca gcc aaa ccc gtt tta ggt gct tta 835
Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro Val Leu Gly Ala Leu
230                235                240                245

cga cgc gcc agc cgc cgc gcc gct ttc ggc gtc gag cgt gac ttc ggg 883
Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val Glu Arg Asp Phe Gly
250                255                260

gag gcc ggg gtg cct cgg gtc taaagatttt gttggcttgc ttc 927
Glu Ala Gly Val Pro Arg Val
265

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<210> 696
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

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Phe Leu Ala Val Leu Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val
20                25                30

Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
35                40                45

Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
50                55                60

Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
65                70                75                80

Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
85                90                95

Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
100               105               110

Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
115               120               125

Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
130               135               140

Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
145               150               155               160

Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
165               170               175

Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
180               185               190

Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
195               200               205

His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu

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tcccactttg cattatcaag ctcaaaaccc gcaccggcga															115
										gtg	ctg	gtc	acc	ggt	
										Val	Leu	Val	Thr	Gly	
										1				5	
gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc															163
Ala	Thr	Gly	Tyr	Ile	Gly	Gly	Arg	Leu	Ile	Thr	Glu	Leu	Leu	Ala	Ala
				10					15					20	
ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc															211
Gly	Phe	Gln	Val	Arg	Ala	Thr	Ser	Arg	Lys	Lys	Thr	Ser	Leu	Gln	Arg
			25					30					35		
ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac															259
Phe	Asp	Trp	Tyr	Glu	Asp	Val	Glu	Ala	Val	Glu	Ala	Asp	Leu	Thr	Asp
		40					45					50			
gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat															307
Ala	Thr	Glu	Leu	Asp	Thr	Leu	Phe	Lys	Asp	Val	Asp	Val	Val	Tyr	Tyr
	55					60					65				
cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag															355
Leu	Val	His	Ser	Met	Gly	Gly	Lys	Asn	Val	Asp	Phe	Glu	Glu	Gln	Glu
70					75					80					85
caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata															403
Gln	Arg	Thr	Ala	Glu	Asn	Val	Ile	Gln	Ala	Ala	Asp	Gln	Ala	Gly	Ile
				90					95					100	
aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata															451
Lys	Gln	Ile	Val	Tyr	Leu	Ser	Gly	Leu	His	Pro	Arg	Asn	Arg	Lys	Ile
		105					110					115			
gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att															499
Glu	Glu	Leu	Ser	Lys	His	Met	Arg	Ser	Arg	Glu	Lys	Val	Ala	Gln	Ile
		120					125					130			

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att	547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile	
135 140 145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag	595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu	
150 155 160 165	
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag	643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu	
170 175 180	
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat	691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp	
185 190 195	
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267

Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly
 375 380 385
 gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405
 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420
 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435
 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450
 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465
 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485
 aaa ctc act taatcgaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 698

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 698

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 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
 130 135 140
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
 145 150 155 160
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
 165 170 175
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
 180 185 190
 Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
 195 200 205
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445

Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
 485

<210> 699

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> FRXA00483

<400> 699

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tcccactttg cattatcaag ctcaaaaccc gcaccggcga gtg ctg gtc acc ggt 115
 Val Leu Val Thr Gly
 1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
 Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
 10 15 20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
 Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
 25 30 35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
 Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
 40 45 50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
 Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
 55 60 65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
 Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
 70 75 80 85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
 Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
 90 95 100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
 Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
 105 110 115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
 Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
 120 125 130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
 Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile

135	140	145	
att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu 150 155 160 165			595
cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu 170 175 180			643
cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp 185 190 195			691
tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser 200 205 210			739
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu 215 220 225			787
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu 230 235 240 245			835
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser 250 255 260			883
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His 265 270 275			931
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr 280 285 290			979
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val 295 300 305			1027
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly 310 315 320 325			1075
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val 330 335 340			1123
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile 345 350 355			1171
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp 360 365 370			1219
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly 375 380 385			1267

gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg 1315
 Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp
 390 395 400 405

 tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca 1363
 Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala
 410 415 420

 gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac 1411
 Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp
 425 430 435

 aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
 Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
 440 445 450

 aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
 Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
 455 460 465

 gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt 1555
 Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
 470 475 480 485

 aaa ctc act taatcgaga gtaggcgtct aaa 1587
 Lys Leu Thr

<210> 700

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

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 20 25 30

 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45

 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60

 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80

 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95

 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110

 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125

 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu

130	135	140
Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile		
145	150	155
Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile		
	165	170
Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu		
	180	185
Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile		
	195	200
Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala		
	210	215
Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu		
	225	230
Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val		
	245	250
Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala		
	260	265
Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp		
	275	280
Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu		
	290	295
Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln		
	305	310
Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala		
	325	330
Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln		
	340	345
Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser		
	355	360
Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly		
	370	375
Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly		
	385	390
Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg		
	405	410
Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile		
	420	425
Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg		
	435	440
Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val		
	450	455
		460

Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
465 470 475 480

Leu Lys Ala Ala Arg Lys Leu Thr
485

<210> 701
<211> 612
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(589)
<223> RXA01534

<400> 701
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Met Thr Ser Ala Ile
1 5

acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163
Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
10 15 20

att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211
Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
25 30 35

ggt tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259
Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
40 45 50

ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307
Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
55 60 65

acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
70 75 80 85

cat gtg cgt aag ctt tct tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
90 95 100

ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
105 110 115

gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
120 125 130

ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547
Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
135 140 145

agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
 Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
 150 155 160

taggacacta aattttaaga ggg 612

<210> 702
 <211> 163
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 702
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 Asn Val Pro Thr Pro Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro
 20 25 30
 Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
 35 40 45
 Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
 50 55 60
 Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
 65 70 75 80
 Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
 85 90 95
 Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
 100 105 110
 Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
 115 120 125
 Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
 130 135 140
 Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
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 Ser Ser Leu

<210> 703
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1111)
 <223> RXA00288

<400> 703
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gat	acc	cct	gat	ccc	act	atg	tct	gct	gtt	gca	atg	tta	gat	tcc	atc	163
Asp	Thr	Pro	Asp	Pro	Thr	Met	Ser	Ala	Val	Ala	Met	Leu	Asp	Ser	Ile	
				10					15					20		
cct	tct	gat	caa	cca	gat	ttc	ctg	atc	gat	gta	gaa	gta	gat	cga	cca	211
Pro	Ser	Asp	Gln	Pro	Asp	Phe	Leu	Ile	Asp	Val	Glu	Val	Asp	Arg	Pro	
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act	ccc	gga	cca	cat	gat	ctg	cta	gtc	cac	att	gag	gcg	gtc	tca	att	259
Thr	Pro	Gly	Pro	His	Asp	Leu	Leu	Val	His	Ile	Glu	Ala	Val	Ser	Ile	
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aac	cct	gtt	gat	acc	aag	gta	cgc	atg	cgg	gcc	ggg	aag	caa	aag	cat	307
Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	Gly	Lys	Gln	Lys	His	
		55					60					65				
cct	aaa	att	tta	ggg	ttt	gat	gct	gca	ggg	gag	gtg	gtg	gct	gtt	gga	355
Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	Val	Val	Ala	Val	Gly	
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tcg	cag	gtc	acg	ctc	ttc	aat	gtt	ggg	gac	aaa	gtg	ttc	tac	gca	gga	403
Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	Val	Phe	Tyr	Ala	Gly	
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tcc	aat	cag	cgt	cca	gga	agt	aac	gca	gag	tac	cag	gtg	gtg	gat	gaa	451
Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	Gln	Val	Val	Asp	Glu	
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cgg	ctg	gtg	ggg	cac	gca	cca	caa	agc	ttg	ggg	gca	cac	gac	gcc	gct	499
Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	Ala	His	Asp	Ala	Ala	
		120					125					130				
gct	ctc	cca	ctt	gtc	gcg	ctc	act	gca	tgg	gag	tca	ctt	ttt	gac	cga	547
Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	Ser	Leu	Phe	Asp	Arg	
		135					140					145				
ttg	gga	gta	act	cag	tca	act	act	gga	aca	ctg	ttg	gtc	ttg	ggc	ggg	595
Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	Leu	Val	Leu	Gly	Gly	
		150					155					160			165	
tca	gga	ggg	gtg	cct	tca	gct	ctt	att	caa	ctt	gct	cga	gct	ctc	act	643
Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	Ala	Arg	Ala	Leu	Thr	
				170							175			180		
ggg	ctg	aaa	gta	gtg	gca	aca	gct	tct	cgc	cct	gaa	tca	caa	gaa	tgg	691
Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	Glu	Ser	Gln	Glu	Trp	
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gtg	aca	aag	ctc	ggg	gct	cat	gag	gtg	att	gat	cac	tcc	aag	gat	ttg	739
Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	His	Ser	Lys	Asp	Leu	
		200							205					210		
agt	gag	caa	atc	tcc	gac	gtg	gat	ttt	gtt	ttc	agc	tcg	tgg	act	act	787
Ser	Glu	Gln	Ile	Ser	Asp	Val	Asp	Phe	Val	Phe	Ser	Ser	Trp	Thr	Thr	
		215					220					225				
ggg	cgt	gaa	gta	gag	ctc	gcc	acg	ttg	atg	aaa	ccc	cag	tcc	cac	cta	835
Gly	Arg	Glu	Val	Glu	Leu	Ala	Thr	Leu	Met	Lys	Pro	Gln	Ser	His	Leu	

230	235	240	245	
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa				883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln	250	255	260	
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc				931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe	265	270	275	
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc				979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala	280	285	290	
gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg				1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu	295	300	305	
gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag				1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu	310	315	320	325
cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac				1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val	330	335		
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<210> 704

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

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Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile				
35	40	45		
Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala				
50	55	60		
Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu				
65	70	75	80	
Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys				
85	90	95		
Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr				
100	105	110		
Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly				
115	120	125		
Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu				
130	135	140		

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
 145 150 155 160
 Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
 165 170 175
 Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
 180 185 190
 Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
 195 200 205
 His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335
 Val

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 <223> RXA02741

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 Met Lys Ala Ile Leu
 1 5
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
 10 15 20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct	211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala	
25 30 35	
ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct	259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala	
40 45 50	
cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag	307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu	
55 60 65	
gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat	355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp	
70 75 80 85	
gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg	403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu	
90 95 100	
gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg	451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu	
105 110 115	
atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt	499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu	
120 125 130	
gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga	547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly	
135 140 145	
ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc	595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser	
150 155 160 165	
gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct	643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala	
170 175 180	
tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg	691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg	
185 190 195	
cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag	739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln	
200 205 210	
tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg	787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val	
215 220 225	
tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag	835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln	
230 235 240 245	
ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc	883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly	
250 255 260	

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
 265 270 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
 280 285 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
 295 300 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320

taaaaagatc ctg 1089

<210> 706
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 706
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Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
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Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
 195 200 205
 Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
 210 215 220
 Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
 225 230 235 240
 Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
 245 250 255
 Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
 260 265 270
 Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
 275 280 285
 Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
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 Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
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 Lys Asp

<210> 707
 <211> 990
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(967)
 <223> RXN02560

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 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65

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att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
70 75 80 85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
90 95 100

atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
105 110 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
120 125 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
135 140 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
150 155 160 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
250 255 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
265 270 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
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attatggacg cct 990

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<210> 708

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

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 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
 260 265 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
 275 280 285

Arg

<210> 709
 <211> 922
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(922)
 <223> FRXA02560

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 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50
 cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65
 att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355
 Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70 75 80 85
 tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg 403
 Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
 90 95 100
 atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg 451
 Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
 105 110 115
 att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa 499
 Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
 120 125 130
 gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
 135 140 145
 ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
 150 155 160 165
 tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg 643
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
 170 175 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260

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 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu
 265 270

<210> 710

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

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 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn
 260 265 270

Gln Glu

<210> 711
 <211> 870
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(847)
 <223> RXA01311

<400> 711
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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
 Met Lys Leu Thr Leu
 1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
 Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
 10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
 Val Gln Val Asp Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
 25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
 Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
 40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
 Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
 55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
 Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala

70	75	80	85	
cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca				403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro				
	90	95	100	
ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc				451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg				
	105	110	115	
tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac				499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn				
	120	125	130	
gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc				547
Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr				
	135	140	145	
gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt				595
Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys				
	150	155	160	165
gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag				643
Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys				
	170	175	180	
ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg				691
Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu				
	185	190	195	
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc				739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys				
	200	205	210	
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg				787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu				
	215	220	225	
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga				835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg				
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ggc aaa gac gac tagtctttaa tccaagtaag tac				870
Gly Lys Asp Asp				

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<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

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Gly	Lys	Phe	Glu	Thr	Val	Gln	Val	Asp	Asp	Ala	Val	Ala	Gln	Met	Ser
			20					25					30		

Ile	Leu	Glu	Leu	Leu	Asp	His	Val	Asn	Asn	Lys	Phe	Ile	Glu	Glu	Gly
		35					40					45			

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110
 Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125
 Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140
 Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160
 Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175
 Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190
 Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205
 Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220
 Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240
 Arg Ala Ala Phe Arg Gly Lys Asp Asp
 245

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<211> 929

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(906)

<223> RXN03014

<400> 713

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 ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg 96
 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30
 gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144

Val	Ser	Met	Ala	Ser	Ser	Met	Val	Phe	Leu	Phe	Gly	Leu	Ala	Met	Val		
		35					40					45					
tac	gcc	tca	gtg	ggc	acg	ttg	aac	atg	gct	cac	gtt	ggc	cta	cgc	atg	192	
Tyr	Ala	Ser	Val	Gly	Thr	Leu	Asn	Met	Ala	His	Val	Gly	Leu	Arg	Met		
	50					55					60						
gaa	gat	gtt	ccg	tct	gga	act	cgc	tcc	gcg	atc	ttc	gca	gtg	ttg	ctc	240	
Glu	Asp	Val	Pro	Ser	Gly	Thr	Arg	Ser	Ala	Ile	Phe	Ala	Val	Leu	Leu		
	65				70					75					80		
gtg	gca	ttc	ggt	att	aaa	gct	gcc	gtg	ttc	ccc	cta	gat	tcc	tgg	ctg	288	
Val	Ala	Phe	Gly	Ile	Lys	Ala	Ala	Val	Phe	Pro	Leu	Asp	Ser	Trp	Leu		
				85					90					95			
ccg	gac	tcc	tac	ccc	acc	gcg	cca	tcg	ctg	gtc	acc	gcg	gtg	ttc	gca	336	
Pro	Asp	Ser	Tyr	Pro	Thr	Ala	Pro	Ser	Leu	Val	Thr	Ala	Val	Phe	Ala		
			100					105					110				
ggt	ctg	ttg	acc	aag	gtg	ggt	gtg	tat	tcc	atc	att	cga	gca	cgc	tcg	384	
Gly	Leu	Leu	Thr	Lys	Val	Gly	Val	Tyr	Ser	Ile	Ile	Arg	Ala	Arg	Ser		
		115				120						125					
att	att	ttc	acc	gat	gga	tcc	ctt	gac	acc	atg	ctg	atg	tgg	gtg	gca	432	
Ile	Ile	Phe	Thr	Asp	Gly	Ser	Leu	Asp	Thr	Met	Leu	Met	Trp	Val	Ala		
		130				135						140					
ctc	gcc	acc	atg	ctc	att	ggt	att	ttg	ggc	gcg	atg	gcg	caa	aac	gat	480	
Leu	Ala	Thr	Met	Leu	Ile	Gly	Ile	Leu	Gly	Ala	Met	Ala	Gln	Asn	Asp		
	145				150					155					160		
atc	aaa	cgt	ttg	ttg	tca	ttt	act	ctg	gtc	agc	cac	atc	ggc	tac	atg	528	
Ile	Lys	Arg	Leu	Leu	Ser	Phe	Thr	Leu	Val	Ser	His	Ile	Gly	Tyr	Met		
				165					170					175			
atc	ttc	ggc	gta	gcc	ctt	gga	tct	gca	cag	ggt	ttg	tct	ggt	gcg	atc	576	
Ile	Phe	Gly	Val	Ala	Leu	Gly	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Ala	Ile		
			180					185					190				
ttc	tac	gca	atc	cac	cac	att	ctg	gtt	cag	act	tcc	ctg	ttc	ctg	gtg	624	
Phe	Tyr	Ala	Ile	His	His	Ile	Leu	Val	Gln	Thr	Ser	Leu	Phe	Leu	Val		
		195					200					205					
gtc	ggt	ctg	gtg	gaa	cgc	caa	gcc	gga	tcc	tcc	tcg	ctg	cga	cgc	ctt	672	
Val	Gly	Leu	Val	Glu	Arg	Gln	Ala	Gly	Ser	Ser	Ser	Leu	Arg	Arg	Leu		
	210					215					220						
gga	tcc	ctg	gca	tat	atc	tcc	cca	ctt	ctt	gcg	att	ttg	tac	ttc	atc	720	
Gly	Ser	Leu	Ala	Tyr	Ile	Ser	Pro	Leu	Leu	Ala	Ile	Leu	Tyr	Phe	Ile		
	225				230					235					240		
ccc	gcc	atc	aac	ctg	ggt	ggt	atc	cca	ccg	ttc	tcc	ggc	ttc	ctg	ggc	768	
Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly		
			245						250					255			
aag	atc	atg	ctc	atc	gaa	gcc	ggc	gcc	cga	aga	tgg	cag	ttg	gct	ggc	816	
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Arg	Arg	Trp	Gln	Leu	Ala	Gly		
		260					265						270				
atg	ggt	cct	tat	cgc	agg	cgc	cgt	tgt	cac	ctc	act	gct	cac	ctt	gta	864	
Met	Gly	Pro	Tyr	Arg	Arg	Arg	Arg	Cys	His	Leu	Thr	Ala	His	Leu	Val		

275 280 285
 cac cat ggt tct ggt ctg gtc caa ggc ctt ctg gcg cga ccg 906
 His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
 290 295 300

 taaagacgcc cccgatggag caa 929

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 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 714
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 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95
 Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110
 Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125
 Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140
 Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160
 Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175
 Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190
 Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205
 Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220
 Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240
 Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly

145	150	155	160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg				528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met				
	165	170	175	
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc				576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile				
	180	185	190	
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg				624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val				
	195	200	205	
gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt				672
Val Gly Leu Val Glu Arg Caa Ala Gly Ser Ser Ser Leu Arg Arg Leu				
	210	215	220	
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc				720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile				
	225	230	235	240
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc				768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly				
	245	250	255	
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca				816
Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala				
	260	265	270	
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac				864
Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr				
	275	280	285	
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac				912
Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp				
	290	295	300	
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat				960
Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp				
	305	310	315	320
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg				1008
Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met				
	325	330	335	
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt				1056
Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu				
	340	345	350	
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc				1104
Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala				
	355	360	365	
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc				1152
Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly				
	370	375	380	
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac				1200
Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp				
	385	390	395	400

245	250	255	
Lys Ile Met Leu Ile Glu Ala Gly	Ala Arg Arg Trp Gln Leu Ala Gly		
260	265	270	
Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr	Ala His Leu Val		
275	280	285	
His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro			
290	295	300	
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Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr			
1	5	10	15
ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg			96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met			
20	25	30	
gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt			144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val			
35	40	45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg			192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met			
50	55	60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc			240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu			
65	70	75	80
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg			288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu			
85	90	95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca			336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala			
100	105	110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg			384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser			
115	120	125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca			432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala			
130	135	140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat			480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp			

gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag 1248
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
 405 410 415

gac caa cca tgatcagtg attcaaacga cga 1280
 Asp Gln Pro

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<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
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Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
 245 250 255
 Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala
 260 265 270
 Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr
 275 280 285
 Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp
 290 295 300
 Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp
 305 310 315 320
 Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met
 325 330 335
 Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu
 340 345 350
 Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala
 355 360 365
 Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly
 370 375 380
 Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp
 385 390 395 400
 Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu
 405 410 415
 Asp Gln Pro

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1051)
 <223> RXN01895

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 Met Ser Val Asn Pro
 1 5
 acc cgc ccc gaa ggc ggc cgt cac cac gtc gtc gtc atc ggt tct ggt 163
 Thr Arg Pro Glu Gly Gly Arg His His Val Val Val Ile Gly Ser Gly
 10 15 20
 ttt ggt ggc ctt ttt gct gcc aag aac ctg gcc aag gca gac gtc gat 211
 Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala Lys Ala Asp Val Asp
 25 30 35

gtc act ctg att gac cgc acc aac cac cac ctc ttc cag cca ctg ctg	259
Val Thr Leu Ile Asp Arg Thr Asn His His Leu Phe Gln Pro Leu Leu	
40 45 50	
tac caa gtg gca acc ggt atc ctc tcc tcc ggt gaa atc gca cct tcc	307
Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly Glu Ile Ala Pro Ser	
55 60 65	
act cga cag atc ctg ggc tcc cag gaa aac gtc aac gtc atc aag ggc	355
Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val Asn Val Ile Lys Gly	
70 75 80 85	
gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg	403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu	
90 95 100	
ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct	451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala	
105 110 115	
ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca	499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala	
120 125 130	
cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc	547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile	
135 140 145	
atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc	595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg	
150 155 160 165	
gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt	643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val	
170 175 180	
gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt	691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly	
185 190 195	
gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat	739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp	
200 205 210	
ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac	787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn	
215 220 225	
gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct	835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala	
230 235 240 245	
atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac	883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp	
250 255 260	
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt	931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly	
265 270 275	

ggt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt 979
 Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val
 280 285 290

gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt 1027
 Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val
 295 300 305

ggc gat cag aag aac gtc ttc gtt 1051
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<213> Corynebacterium glutamicum

<400> 718

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Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
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Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
 50 55 60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
 65 70 75 80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
 85 90 95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
 100 105 110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
 115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
 130 135 140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
 145 150 155 160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
 165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
 180 185 190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
 195 200 205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
 210 215 220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
 225 230 235 240
 Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
 245 250 255
 Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
 260 265 270
 Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
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 Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn
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 Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
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 Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
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 gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144
 Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
 35 40 45
 tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192
 Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
 50 55 60
 tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240
 Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
 65 70 75 80
 aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288
 Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
 85 90 95
 gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336
 Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
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 atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt 384
 Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

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gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432
Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
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Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145 150 155 160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528
Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
165 170 175

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Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
180 185 190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624
Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
195 200 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672
Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
210 215 220

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Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
225 230 235 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768
Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
245 250 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816
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<213> Corynebacterium glutamicum

<400> 720

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Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
65 70 75 80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
85 90 95

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Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
 130 135 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
 145 150 155 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
 165 170 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
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Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
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 <223> RXA00703

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 Met Thr Thr Pro Pro
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act gag att tcg aac gtg aat ccc acc gcg aat gaa ttt gat gat ccg 163
 Thr Glu Ile Ser Asn Val Asn Pro Thr Ala Asn Glu Phe Asp Asp Pro
 10 15 20

gat gtg gga cgg cgc att act tct gct gct ggt gtg cca ggc gtt ttg 211
 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu

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His	Ala	Leu	Gln	His	Ala	Val	Pro	Asn	Arg	Ala	Leu	Leu	Pro	Leu	Leu			
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acc	atg	aat	aaa	cca	ggc	ggc	atc	gac	tgt	cct	ggt	tgt	gct	tgg	cct	307		
Thr	Met	Asn	Lys	Pro	Gly	Gly	Ile	Asp	Cys	Pro	Gly	Cys	Ala	Trp	Pro			
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gag	cct	tcc	act	gcc	aac	ctt	ggt	gtg	gtt	gag	ttc	tgc	gag	aac	ggt	355		
Glu	Pro	Ser	Thr	Ala	Asn	Leu	Gly	Val	Val	Glu	Phe	Cys	Glu	Asn	Gly			
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gcc	aag	gcg	gtc	gcc	gag	gaa	aca	aca	cct	gat	cgt	gcc	ggc	aaa	gag	403		
Ala	Lys	Ala	Val	Ala	Glu	Glu	Thr	Thr	Pro	Asp	Arg	Ala	Gly	Lys	Glu			
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Phe	Trp	Ala	Glu	His	Ser	Ile	Tyr	Asp	Leu	Arg	Glu	Lys	Thr	Asp	His			
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tgg	ctg	gga	aag	cgt	ggc	cga	atc	acc	gag	ccc	atg	ttt	tat	gat	cgt	499		
Trp	Leu	Gly	Lys	Arg	Gly	Arg	Ile	Thr	Glu	Pro	Met	Phe	Tyr	Asp	Arg			
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tct	tct	ggc	gat	gat	cac	tac	cgc	cct	att	tct	tgg	gat	cgt	gca	ttt	547		
Ser	Ser	Gly	Asp	Asp	His	Tyr	Arg	Pro	Ile	Ser	Trp	Asp	Arg	Ala	Phe			
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gcg	atc	att	gcg	tcg	aag	ctc	cgc	gag	atc	gag	cca	gat	gaa	gcg	gtg	595		
Ala	Ile	Ile	Ala	Ser	Lys	Leu	Arg	Glu	Ile	Glu	Pro	Asp	Glu	Ala	Val			
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Phe	Tyr	Thr	Ser	Gly	Arg	Ala	Pro	Asn	Glu	Pro	Ala	Tyr	Met	Leu	Gln			
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ctt	cta	gcc	cgc	cga	ctt	ggc	aca	aat	aat	ctt	cca	gac	tgt	gga	aac	691		
Leu	Leu	Ala	Arg	Arg	Leu	Gly	Thr	Asn	Asn	Leu	Pro	Asp	Cys	Gly	Asn			
			185					190					195					
atg	tgc	cac	gag	tcc	acc	ggt	act	gcc	ttg	ggt	gag	acc	ttg	ggt	ttg	739		
Met	Cys	His	Glu	Ser	Thr	Gly	Thr	Ala	Leu	Gly	Glu	Thr	Leu	Gly	Leu			
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Gly	Lys	Gly	Ser	Val	Val	Met	Glu	Asp	Phe	Tyr	Asn	Thr	Asp	Leu	Leu			
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Ile	Ser	Val	Gly	Gln	Asn	Pro	Gly	Thr	Asn	His	Pro	Arg	Ala	Leu	Thr			
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gct	ttc	aaa	gaa	ttg	aag	gaa	aac	ggt	ggc	aag	att	ctg	gcg	ctg	aac	883		
Ala	Phe	Lys	Glu	Leu	Lys	Glu	Asn	Gly	Gly	Lys	Ile	Leu	Ala	Leu	Asn			
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ccc	atg	cca	gag	acc	ggt	ctg	atg	aaa	ttc	cgt	gag	ccc	caa	tca	gtc	931		
Pro	Met	Pro	Glu	Thr	Gly	Leu	Met	Lys	Phe	Arg	Glu	Pro	Gln	Ser	Val			
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Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala Asp Glu Tyr Leu Gln	
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atc cgt ctt gat gga gac cgc gca ttc ttc cag gcg ctc aac aag gaa	1027
Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln Ala Leu Asn Lys Glu	
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Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe Leu Asp Lys Phe Cys	
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Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys Ser Leu Asp Asp Glu	
330 335 340	
gtt ctg ctc aag gga tgc ggt ctg acg gca gcg gag atc aac aag gcc	1171
Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala Glu Ile Asn Lys Ala	
345 350 355	
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Ala Asp Met Val Glu Lys Ser Asp Thr Val Val Val Ser Trp Thr Leu	
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Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr Ile Arg Glu Met Val	
375 380 385	
aac ttc ctg ctg ctt act gga aat att ggt aag cct ggc gca ggc act	1315
Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys Pro Gly Ala Gly Thr	
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gcc ccg ctt cgt ggg cac tca aac gtc cag ggt gat cga acc atg ggt	1363
Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly	
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Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu	
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Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe Asp Thr Val Asn Ser	
440 445 450	
ctg cga gcc atg cgc gaa ggc aag acc aag ttc ttt ctc tcc ctc ggt	1507
Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe Phe Leu Ser Leu Gly	
455 460 465	
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Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser Val Val Glu Lys Gly	
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atg gaa tcc aat gag ctg acg gtg cat ctg tcg acc aag ccc aat ggt	1603
Met Glu Ser Asn Glu Leu Thr Val His Leu Ser Thr Lys Pro Asn Gly	
490 495 500	
tca caa gca tgg cct ggt gag cag tca ctt atc ctt ccg gtg att gct	1651
Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile Leu Pro Val Ile Ala	
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cga aca gat aag gat gtc caa aag tca ggc gtc cag cgt gtg aca gtt	1699
Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val Gln Arg Val Thr Val	
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gag gat tct gcc ggc gct gtt cac gca tcc act ggt aaa cga acc gcc	1747
Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr Gly Lys Arg Thr Ala	
535 540 545	
aac aag gat ctg aat ttg aag tcc gaa tgc gac atc att gga acc atc	1795
Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp Ile Ile Gly Thr Ile	
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Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln Pro Met Ile Asp Asn	
570 575 580	
tac gat gtg gtc cgc gat cac atc gag gcc acc att cct ggg ttc cac	1891
Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr Ile Pro Gly Phe His	
585 590 595	
gat ttc aac cgt cgc atc gac aac ccc ggt gga ttc ctc ctc ccc aac	1939
Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly Phe Leu Leu Pro Asn	
600 605 610	
gga cct cgt gag cgc atc ttc aac aca tcc aat ggc aag gcc caa ttg	1987
Gly Pro Arg Glu Arg Ile Phe Asn Thr Ser Asn Gly Lys Ala Gln Leu	
615 620 625	
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Thr Val Asn Glu Thr Asn Val Ile Glu Leu Pro Lys Asp Tyr Leu Leu	
630 635 640 645	
atg aac acg gta cgt tca cat gat caa tac aac tcc acg att tac ggt	2083
Met Asn Thr Val Arg Ser His Asp Gln Tyr Asn Ser Thr Ile Tyr Gly	
650 655 660	
ctg gat gac cgc tac cgc ggt gtt cgc aat ggt cgc cgc gta gtg ttc	2131
Leu Asp Asp Arg Tyr Arg Gly Val Arg Asn Gly Arg Arg Val Val Phe	
665 670 675	
gtc aat cct caa gat tgt aag caa cgt ggt ctc aag gat gga gac atc	2179
Val Asn Pro Gln Asp Cys Lys Gln Arg Gly Leu Lys Asp Gly Asp Ile	
680 685 690	
gtc gat atc gtc tct gtc ttt gat gat ggc gaa cgc cga gca ccg aat	2227
Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu Arg Arg Ala Pro Asn	
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ttc cga gtg gtg gaa tat gac acc gcg agg gac tgc gtc acc acg tat	2275
Phe Arg Val Val Glu Tyr Asp Thr Ala Arg Asp Cys Val Thr Thr Tyr	
710 715 720 725	
ttc cct gag gcc aac gta ttg gtt cca ttg gat tca gta gct gaa aaa	2323
Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp Ser Val Ala Glu Lys	
730 735 740	
tcc aac act cca gtg tcc aag tca gtt gtg gtt cgc ctt gaa gca aca	2371
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Gly Arg Thr Ala Ser
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<211> 762

<212> PRT

<213> Corynebacterium glutamicum

<400> 722

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Val Pro Gly Val Leu His Ala Leu Gln His Ala Val Pro Asn Arg Ala
35 40 45

Leu Leu Pro Leu Leu Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro
50 55 60

Gly Cys Ala Trp Pro Glu Pro Ser Thr Ala Asn Leu Gly Val Val Glu
65 70 75 80

Phe Cys Glu Asn Gly Ala Lys Ala Val Ala Glu Glu Thr Thr Pro Asp
85 90 95

Arg Ala Gly Lys Glu Phe Trp Ala Glu His Ser Ile Tyr Asp Leu Arg
100 105 110

Glu Lys Thr Asp His Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro
115 120 125

Met Phe Tyr Asp Arg Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser
130 135 140

Trp Asp Arg Ala Phe Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu
145 150 155 160

Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro
165 170 175

Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu
180 185 190

Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly
195 200 205

Glu Thr Leu Gly Leu Gly Lys Gly Ser Val Val Met Glu Asp Phe Tyr
210 215 220

Asn Thr Asp Leu Leu Ile Ser Val Gly Gln Asn Pro Gly Thr Asn His
225 230 235 240

Pro Arg Ala Leu Thr Ala Phe Lys Glu Leu Lys Glu Asn Gly Gly Lys
245 250 255

Ile Leu Ala Leu Asn Pro Met Pro Glu Thr Gly Leu Met Lys Phe Arg
260 265 270

Glu Pro Gln Ser Val Lys Gly Ala Leu Ser Ile Ser Asp Lys Leu Ala
 275 280 285
 Asp Glu Tyr Leu Gln Ile Arg Leu Asp Gly Asp Arg Ala Phe Phe Gln
 290 295 300
 Ala Leu Asn Lys Glu Leu Ile Arg Arg Asp Ala Leu Asp His Ala Phe
 305 310 315 320
 Leu Asp Lys Phe Cys Ser Gly Val Asp Glu Thr Ile Glu His Leu Lys
 325 330 335
 Ser Leu Asp Asp Glu Val Leu Leu Lys Gly Cys Gly Leu Thr Ala Ala
 340 345 350
 Glu Ile Asn Lys Ala Ala Asp Met Val Glu Lys Ser Asp Thr Val Val
 355 360 365
 Val Ser Trp Thr Leu Gly Val Thr Gln His Lys Asn Ala Val Tyr Thr
 370 375 380
 Ile Arg Glu Met Val Asn Phe Leu Leu Leu Thr Gly Asn Ile Gly Lys
 385 390 395 400
 Pro Gly Ala Gly Thr Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly
 405 410 415
 Asp Arg Thr Met Gly Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala
 420 425 430
 Ala Leu Glu Asn Glu Phe Gly Phe Asp Val Pro Arg Lys His Gly Phe
 435 440 445
 Asp Thr Val Asn Ser Leu Arg Ala Met Arg Glu Gly Lys Thr Lys Phe
 450 455 460
 Phe Leu Ser Leu Gly Gly Asn Leu Val Arg Val Ser Ser Asp Thr Ser
 465 470 475 480
 Val Val Glu Lys Gly Met Glu Ser Asn Glu Leu Thr Val His Leu Ser
 485 490 495
 Thr Lys Pro Asn Gly Ser Gln Ala Trp Pro Gly Glu Gln Ser Leu Ile
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 Leu Pro Val Ile Ala Arg Thr Asp Lys Asp Val Gln Lys Ser Gly Val
 515 520 525
 Gln Arg Val Thr Val Glu Asp Ser Ala Gly Ala Val His Ala Ser Thr
 530 535 540
 Gly Lys Arg Thr Ala Asn Lys Asp Leu Asn Leu Lys Ser Glu Cys Asp
 545 550 555 560
 Ile Ile Gly Thr Ile Gly Lys Gln Thr Phe Gly Asp Ala Phe Trp Gln
 565 570 575
 Pro Met Ile Asp Asn Tyr Asp Val Val Arg Asp His Ile Glu Ala Thr
 580 585 590
 Ile Pro Gly Phe His Asp Phe Asn Arg Arg Ile Asp Asn Pro Gly Gly

1032

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Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr	
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Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly	
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cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc	403
Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro	
90 95 100	
aaa gac aat ccg gcc cgg gat ccc gtc cag aat ccc tcc cat aat ccc	451
Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro	
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gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta	499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val	
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cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct	547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser	
135 140 145	
gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag	595
Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys	
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aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg	643
Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val	
170 175 180	
tcg ttg cca gat aag ttg aag tcg aag cag aag att ttc gac aaa act	691
Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr	
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Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu	
200 205 210	
att att cga gag gat gtc ggt cgg cat aac gca gct gac aaa gtt ata	787
Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile	
215 220 225	
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230 235 240 245	
gtg atg agt tct agg gcg tct ttt gag ctt gtc caa aag gct gcc atg	883
Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met	
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Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala	
265 270 275	
atc gag gcg gcg cag gat tca ggt att ttc ctt gct ggt ttt gtt cgg	979
Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg	
280 285 290	

ggc aac aag ttt aac cac tat gcg ggc gag ctc gga taatgccaga 1025
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 295 300 305

acaggtagaa cag 1038

<210> 724

<211> 305

<212> PRT

<213> Corynebacterium glutamicum

<400> 724

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Asp Glu Gln Val Phe Val Asn Thr Arg Pro Asp Thr Val Ala Val Glu
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Glu Pro Leu Glu Ile Arg Val Asn Gly Thr Ala Leu Thr Thr Thr Met
 35 40 45

Arg Thr Pro Gly His Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser
 50 55 60

Glu Gly Leu Ile Thr Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys
 65 70 75 80

Ala Gly Ala Val Gly Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu
 85 90 95

Leu Asp Val Ile Pro Lys Asp Asn Pro Ala Arg Asp Pro Val Gln Asn
 100 105 110

Pro Ser His Asn Pro Glu Gly Ser Gln His Glu Ala Leu His Ile Pro
 115 120 125

Thr Phe Gln Pro Val Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn
 130 135 140

Val Leu Thr Thr Ser Ala Cys Gly Val Cys Gly Thr Thr Ser Ile Glu
 145 150 155 160

Gln Leu Met Asn Lys Lys Gly Trp Pro Ile Thr Pro Ile Thr Pro Asp
 165 170 175

Pro Arg Met Ile Val Ser Leu Pro Asp Lys Leu Lys Ser Lys Gln Lys
 180 185 190

Ile Phe Asp Lys Thr Gly Gly Val His Ala Ala Gly Leu Ala Thr Leu
 195 200 205

Asp Gly Glu Met Leu Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala
 210 215 220

Ala Asp Lys Val Ile Gly Asn Met Leu Met Ala Gly Lys Leu Pro Leu
 225 230 235 240

Glu Asn Thr Ile Leu Val Met Ser Ser Arg Ala Ser Phe Glu Leu Val
 245 250 255

Gln Lys Ala Ala Met Ala Gly Ile Ser Gly Val Ile Ala Val Gly Ala
 260 265 270

Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln Asp Ser Gly Ile Phe Leu
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Ala Gly Phe Val Arg Gly Asn Lys Phe Asn His Tyr Ala Gly Glu Leu
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Gly
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<211> 908

<212> DNA

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<220>

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<223> FRXA00705

<400> 725

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gat act gtt gcg gtg gag gag cct cta gaa att cgg gtt aat ggc act 96
 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
 20 25 30

gcg ctt acc acc act atg cgc acg ccc ggc cat gat att gag ttg gtg 144
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45

cat ggc ctc ctc ttg tca gaa ggt ctg atc acg gat gct tct gag gtt 192
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
 50 55 60

ttt acc gcc cgc tat tgt gca gga gct gtt ggc cca gat aat caa aat 240
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65 70 75 80

acg tac aac gtc tta gaa ctt gat gtc atc ccc aaa gac aat ccg gcc 288
 Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro Lys Asp Asn Pro Ala
 85 90 95

cgg gat ccc gtc cag aat ccc tcc cat aat ccc gaa ggc agc caa cac 336
 Arg Asp Pro Val Gln Asn Pro Ser His Asn Pro Glu Gly Ser Gln His
 100 105 110

gaa gca ctc cac atc cca act ttc caa ccg gta cgc gaa cta aac ctc 384
 Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val Arg Glu Leu Asn Leu
 115 120 125

gtg gca gcc caa cgc aat gtg ctg act acg tct gct tgt ggt gtt tgt 432
 Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser Ala Cys Gly Val Cys
 130 135 140

ggc acg acg tct att gag cag ttg atg aac aag aag ggc tgg ccc att 480

Gly Thr Thr Ser Ile Glu Gln Leu Met Asn Lys Lys Gly Trp Pro Ile
 145 150 155 160
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
 165 170 175
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
 180 185 190
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp
 195 200 205
 gtc ggt ccg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg 672
 Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met
 210 215 220
 gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg 720
 Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg
 225 230 235 240
 gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt 768
 Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly
 245 250 255
 gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag 816
 Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln
 260 265 270
 gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac 864
 Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn
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 cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag 908
 His Tyr Ala Gly Glu Leu Gly
 290 295

<210> 726

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

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 20 25 30
 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
 35 40 45
 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
 50 55 60
 Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly Pro Asp Asn Gln Asn
 65 70 75 80

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acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115
                                         Met Leu Pro Val Asn
                                         1           5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg qca tac atc 163

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Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile	
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atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa	211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln	
25 30 35	
caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc	259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu	
40 45 50	
gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac	307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp	
55 60 65	
atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa	355
Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu	
70 75 80 85	
acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc	403
Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly	
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gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc	451
Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser	
105 110 115	
cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc	499
Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu	
120 125 130	
ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc	547
Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg	
135 140 145	
gtg gta tgg cca tgg atc ctc acc cca atg ctg gca ctg ctc ttc tac	595
Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu Ala Leu Leu Phe Tyr	
150 155 160 165	
ggt ggc acc cag ctg tac tcc gac gca gca cca gtc gtt cca gca ctg	643
Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro Val Val Pro Ala Leu	
170 175 180	
cag tcc ttc tgg ttc ccg atc cac gtt tcc tcc gtc tcc atc ggc gca	691
Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser Val Ser Ile Gly Ala	
185 190 195	
tcc atc ggt atc gtc tcc ggt att gca tcc ctg ctg tac ata ctg cgc	739
Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu Leu Tyr Ile Leu Arg	
200 205 210	
atg tgg caa cca aag ggt aaa gaa aag ggc ttc ttc ggc gca gta gca	787
Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe Phe Gly Ala Val Ala	
215 220 225	
aaa cca ctc cca tcc gga aaa acc ctg gat aac ctg gca tac aag acc	835
Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn Leu Ala Tyr Lys Thr	
230 235 240 245	
gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc	883
Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala	

	250	255	260	
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Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys				
	265	270	275	
gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac				979
Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His				
	280	285	290	
gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac				1027
Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn				
	295	300	305	
atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg				1075
Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met				
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gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt				1121
Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn				
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tggttggcgg ggt				1134
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Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr				
35 40 45				
Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr				
50 55 60				
Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu				
65 70 75 80				
Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser				
85 90 95				
Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg				
100 105 110				
Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile				
115 120 125				
Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln				
130 135 140				
Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu				
145 150 155 160				

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro
 165 170 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser
 180 185 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu
 195 200 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe
 210 215 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn
 225 230 235 240

Leu Ala Tyr Lys Thr Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly
 245 250 255

Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp
 260 265 270

Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr
 275 280 285

Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn
 290 295 300

Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met Ile Phe Asn Leu
 305 310 315 320

Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu
 325 330 335

Asn

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 <223> FRXA00388

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ttc ggc ctg ggc atc atc ttg ggt gcc atc tgg gca gaa gca gcc tgg 96
 Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
 20 25 30

ggt cgt ttc tgg gga tgg gat cct aag gaa aca gtc tcc ttc atc acc 144
 Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
 35 40 45

tgg gtt ctc tac gct ggt tac ctc cac gca cgt gca act gct ggt tgg 192

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

cgc aac acc aac gct gca tgg atc aac atc ctg gcg ctg gtc acg atg 240
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

att ttt aat ctg ttc ttc atc aac atg gtc gta tct ggt ctg cac tct 288
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

tac gcc gga ctg aac taagcacttt tgggtggcgg ggt 326
 Tyr Ala Gly Leu Asn
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<210> 730
 <211> 101
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<400> 730
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Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
 35 40 45

Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60

Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80

Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95

Tyr Ala Gly Leu Asn
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 <213> Corynebacterium glutamicum

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 <223> FRXA00386

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 Met Leu Pro Val Asn
 1 5

caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163
 Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
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 atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211
 Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
 25 30 35

 caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259
 Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
 40 45 50

 gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307
 Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
 55 60 65

 atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355
 Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
 70 75 80 85

 acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403
 Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
 90 95 100

 gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451
 Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
 105 110 115

 cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499
 Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
 120 125 130

 ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547
 Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
 135 140 145

 gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595
 Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser
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 Thr Val Ala Pro Ser
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<210> 732

<211> 170

<212> PRT

<213> *Corynebacterium glutamicum*

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 Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
 35 40 45

 Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr

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Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly	
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Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala	
105 110 115	
ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca	499
Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala	
120 125 130	
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Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met	
135 140 145	
ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc	595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe	
150 155 160 165	
ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta	643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val	
170 175 180	
tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc	691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile	
185 190 195	
gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc	739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala	
200 205 210	
ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc	787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile	
215 220 225	
tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc	835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe	
230 235 240 245	
acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc	883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile	
250 255 260	
gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca	931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro	
265 270 275	
atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg	979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu	
280 285 290	
ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt	1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu	
295 300 305	
gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc	1072
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310 315 320	
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<210> 734

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35           40           45

Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50           55           60

His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65           70           75           80

Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
 85           90           95

Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
100           105           110

Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
115           120           125

Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
130           135           140

Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
145           150           155           160

Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
165           170           175

Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
180           185           190

Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
195           200           205

Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
210           215           220

Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
225           230           235           240

Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
245           250           255

Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
260           265           270

Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
275           280           285

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Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
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Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
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Lys Ala Asn Ala

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<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN02556

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 Leu Ile Val Ser Thr
 1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
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atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
 70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
 Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
 90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
 Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
 105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
 Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
 120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547

Val	Ala	Glu	Ala	Trp	Asp	Ala	Val	Tyr	Trp	Ile	Met	Ala	Asn	Val	Leu		
135						140					145						
atc	ggt	ttt	gag	aac	aac	ctt	tat	gct	tcc	aac	gat	ctg	gag	cct	ggc	595	
Ile	Gly	Phe	Glu	Asn	Asn	Leu	Tyr	Ala	Ser	Asn	Asp	Leu	Glu	Pro	Gly		
150					155					160					165		
gac	gtc	ttc	cgc	gaa	gtc	acc	gtg	acc	gcg	aag	aag	cag	ctc	agc	gca	643	
Asp	Val	Phe	Arg	Glu	Val	Thr	Val	Thr	Ala	Lys	Lys	Gln	Leu	Ser	Ala		
				170					175					180			
acc	gtc	tgg	gaa	tac	acc	ctg	gca	ggt	gag	ctg	ggt	gcc	cca	gag	cca	691	
Thr	Val	Trp	Glu	Tyr	Thr	Leu	Ala	Gly	Glu	Leu	Val	Ala	Pro	Glu	Pro		
			185					190					195				
ggt	cag	tac	acc	tcc	atc	gga	gta	gtg	ctt	gac	gac	ggc	gcc	cgc	cag	739	
Gly	Gln	Tyr	Thr	Ser	Ile	Gly	Val	Val	Leu	Asp	Asp	Gly	Ala	Arg	Gln		
	200					205						210					
ctg	cgc	cag	tac	agc	ttg	ctc	ggc	ggc	tcc	gac	acc	gag	tac	cgc	att	787	
Leu	Arg	Gln	Tyr	Ser	Leu	Leu	Gly	Gly	Ser	Asp	Thr	Glu	Tyr	Arg	Ile		
	215					220					225						
gcg	gtt	gag	gat	aac	ggc	gag	gtt	tct	gga	ttc	ctg	cgt	gat	cgc	gta	835	
Ala	Val	Glu	Asp	Asn	Gly	Glu	Val	Ser	Gly	Phe	Leu	Arg	Asp	Arg	Val		
230					235				240						245		
tcc	gtt	ggt	gac	aag	att	gaa	gcc	acc	atc	gcg	gcc	ggc	gac	ctg	gtt	883	
Ser	Val	Gly	Asp	Lys	Ile	Glu	Ala	Thr	Ile	Ala	Ala	Gly	Asp	Leu	Val		
				250					255					260			
ctt	aac	aag	gac	acc	aat	cca	gtt	gtg	ctg	att	tcc	cag	ggc	atc	ggc	931	
Leu	Asn	Lys	Asp	Thr	Asn	Pro	Val	Val	Leu	Ile	Ser	Gln	Gly	Ile	Gly		
			265					270					275				
tcc	acc	cca	atg	gtg	ggc	atg	ctc	gca	ggt	atg	aac	cct	gaa	cgt	gac	979	
Ser	Thr	Pro	Met	Val	Gly	Met	Leu	Ala	Gly	Met	Asn	Pro	Glu	Arg	Asp		
		280					285					290					
gtt	gtg	gtt	ttg	cat	gct	gac	cag	gcc	gag	tcc	acc	tac	gcg	cag	gtg	1027	
Val	Val	Val	Leu	His	Ala	Asp	Gln	Ala	Glu	Ser	Thr	Tyr	Ala	Gln	Val		
	295					300					305						
gag	gaa	gtg	cag	ggg	ctc	gtc	gaa	aag	ctc	cct	aag	gct	gcg	ttt	gaa	1075	
Glu	Glu	Val	Gln	Gly	Leu	Val	Glu	Lys	Leu	Pro	Lys	Ala	Ala	Phe	Glu		
310					315					320					325		
atc	ttc	tac	cgc	gac	aac	gac	cag	tgg	ctc	gag	gtc	gct	ggc	cgc	att	1123	
Ile	Phe	Tyr	Arg	Asp	Asn	Asp	Gln	Trp	Leu	Glu	Val	Ala	Gly	Arg	Ile		
				330					335					340			
cca	tca	ggt	gcg	tcc	gtg	tac	ctg	tgc	ggt	ggc	gtg	gaa	ttc	ttg	aag	1171	
Pro	Ser	Gly	Ala	Ser	Val	Tyr	Leu	Cys	Gly	Gly	Val	Glu	Phe	Leu	Lys		
			345					350					355				
aac	gtg	cgt	gag	cag	atc	gag	gcg	ctc	gat	gag	cag	cct	cgc	gac	gta	1219	
Asn	Val	Arg	Glu	Gln	Ile	Glu	Ala	Leu	Asp	Glu	Gln	Pro	Arg	Asp	Val		
		360					365					370					
aac	ttc	gag	ctc	ttc	gca	cca	aac	gac	tgg	ctg	att	tcc	taagcccaca			1268	
Asn	Phe	Glu	Leu	Phe	Ala	Pro	Asn	Asp	Trp	Leu	Ile	Ser					

375

380

385

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1281

<210> 736

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

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Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380

Ile Ser
 385

<210> 737
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1258)
 <223> FRXA02556

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gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
 Leu Ile Val Ser Thr
 1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
 Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
 10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
 Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
 25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
 Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
 40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307
 Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
 55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
 Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp

70	75	80	85	
gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val	90	95	100	403
tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu	105	110	115	451
ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro	120	125	130	499
gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu	135	140	145	547
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly	150	155	160	595
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala	170	175	180	643
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro	185	190	195	691
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln	200	205	210	739
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile	215	220	225	787
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val	230	235	240	835
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val	250	255	260	883
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly	265	270	275	931
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp	280	285	290	979
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val	295	300	305	1027
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu	310	315	320	1075

atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att 1123
 Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile
 330 335 340

cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag 1171
 Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys
 345 350 355

aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta 1219
 Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val
 360 365 370

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385

ccccgaaact tcc 1281

<210> 738
 <211> 386
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 738
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 Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335
 Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350
 Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365
 Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380
 Ile Ser
 385

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 <212> DNA
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 <222> (101)..(1177)
 <223> RXA01392

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 ttgacatatc atctaaattt ccaagagagg acaccacaca gtg gct aac acg tca 115
 Val Ala Asn Thr Ser
 1 5
 tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe
 10 15 20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca	211
Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro	
25 30 35	
gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct	259
Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro	
40 45 50	
gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg	307
Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp	
55 60 65	
gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
70 75 80 85	
atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act	403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
90 95 100	
ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
105 110 115	
cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
150 155 160 165	
cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
215 220 225	
cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	

tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg 931
 Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu
 265 270 275

 cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc 979
 Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr
 280 285 290

 gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc 1027
 Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr
 295 300 305

 cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac 1075
 Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His
 310 315 320 325

 ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg 1123
 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu
 330 335 340

 cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt 1171
 Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys Asn Pro Glu Pro Phe
 345 350 355

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 Gln Lys

<210> 740

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 740

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 20 25 30

 Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly
 35 40 45

 Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala
 50 55 60

 Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu
 65 70 75 80

 Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp
 85 90 95

 Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val
 100 105 110

 Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp
 115 120 125

 Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys
 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu
 145 150 155 160
 Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala
 165 170 175
 Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu
 180 185 190
 Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala
 195 200 205
 His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu
 210 215 220
 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu
 225 230 235 240
 Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr
 245 250 255
 His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn
 260 265 270
 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp
 275 280 285
 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala
 290 295 300
 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly
 305 310 315 320
 Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala
 325 330 335
 Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys
 340 345 350
 Asn Pro Glu Pro Phe Gln Lys
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<210> 741
 <211> 1227
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1204)
 <223> RXA00800

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 Met Ser Thr Val Val
 1 5

cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac	163
Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn	
10 15 20	
ggt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag	211
Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln	
25 30 35	
gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att	259
Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile	
40 45 50	
tca gat gag ttc cct tac ctc ctc ggc cac gag gca gca ggc att gtt	307
Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu Ala Ala Gly Ile Val	
55 60 65	
gag gag gta ggc gag tcc gtc acc cac gtt gag gtc ggc gat ttc gtc	355
Glu Glu Val Gly Glu Ser Val Thr His Val Glu Val Gly Asp Phe Val	
70 75 80 85	
atc ttg aac tgg cgt gca gtg tgc ggc gag tgc cgt gca tgt aag aag	403
Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys Arg Ala Cys Lys Lys	
90 95 100	
ggc gag cca aag tac tgc ttt aac acc cac aac gcc tct aag aag atg	451
Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn Ala Ser Lys Lys Met	
105 110 115	
acc ctg gaa gac ggc acc gag ctg tcc cca gca ctg ggt att ggc gcg	499
Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala Leu Gly Ile Gly Ala	
120 125 130	
ttc ttg gaa aag acc ctg gtc cac gaa ggc cag tgc acc aag gtt aac	547
Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln Cys Thr Lys Val Asn	
135 140 145	
cct gag gaa gat cca gca gca gct ggc ctt ctg ggt tgt ggc atc atg	595
Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu Gly Cys Gly Ile Met	
150 155 160 165	
gca ggc ctt ggc gct gcg gtg aac acc ggt gat att aag cgt ggc gag	643
Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp Ile Lys Arg Gly Glu	
170 175 180	
tcc gta gca gtc ttc ggc ctt ggt ggc gtg ggc atg gca gct att gct	691
Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly Met Ala Ala Ile Ala	
185 190 195	
ggc gcc aag att gct ggc gct tcc aag atc att gct gtt gat atc gat	739
Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile Ala Val Asp Ile Asp	
200 205 210	
gag aag aag ctg gag tgg gcg aag gaa ttc ggc gca acc cac acc att	787
Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly Ala Thr His Thr Ile	
215 220 225	
aat tcc tct ggt ctt ggt ggc gaa ggt gat gcc tct gag gtc gtg gca	835
Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala Ser Glu Val Val Ala	
230 235 240 245	
aag gtt cgt gag ctc acc gat ggt ttc ggc acc gat gtc tcc atc gat	883

Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr Asp Val Ser Ile Asp
 250 255 260

gcg gta ggc atc atg ccg acc tgg cag cag gcg ttt tac tcc cgt gac 931
 Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala Phe Tyr Ser Arg Asp
 265 270 275

cat gca ggc cgc atg gtg atg gtg ggc gtt cca aac ctg acg tct cgc 979
 His Ala Gly Arg Met Val Met Val Gly Val Pro Asn Leu Thr Ser Arg
 280 285 290

gta gat gtt cct gcg att gat ttt tac ggt cgc ggt gga tcc gtg cgc 1027
 Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg Gly Gly Ser Val Arg
 295 300 305

cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat 1075
 Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr
 310 315 320 325

gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct 1123
 Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser
 330 335 340

gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag 1171
 Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys
 345 350 355

gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224
 Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
 360 365

gcg 1227

<210> 742
 <211> 368
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 742
 Met Ser Thr Val Val Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro
 1 5 10 15

Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val
 20 25 30

Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr
 35 40 45

Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu
 50 55 60

Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu
 65 70 75 80

Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys
 85 90 95

Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn
 100 105 110

Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala
 115 120 125
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln
 130 135 140
 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu
 145 150 155 160
 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp
 165 170 175
 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly
 180 185 190
 Met Ala Ala Ile Ala Gly Ala Lys Ile Ala Gly Ala Ser Lys Ile Ile
 195 200 205
 Ala Val Asp Ile Asp Glu Lys Lys Leu Glu Trp Ala Lys Glu Phe Gly
 210 215 220
 Ala Thr His Thr Ile Asn Ser Ser Gly Leu Gly Gly Glu Gly Asp Ala
 225 230 235 240
 Ser Glu Val Val Ala Lys Val Arg Glu Leu Thr Asp Gly Phe Gly Thr
 245 250 255
 Asp Val Ser Ile Asp Ala Val Gly Ile Met Pro Thr Trp Gln Gln Ala
 260 265 270
 Phe Tyr Ser Arg Asp His Ala Gly Arg Met Val Met Val Gly Val Pro
 275 280 285
 Asn Leu Thr Ser Arg Val Asp Val Pro Ala Ile Asp Phe Tyr Gly Arg
 290 295 300
 Gly Gly Ser Val Arg Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg
 305 310 315 320
 Asp Phe Pro Thr Tyr Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu
 325 330 335
 Asp Lys Phe Val Ser Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala
 340 345 350
 Phe Asn Thr Met Lys Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
 355 360 365

<210> 743
 <211> 1011
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(988)
 <223> RXA02143

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 215 220 225

aac atg cct aag ttc tcc gat cgt cag ctc tcc gca gat gag aag aag 835
 Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser Ala Asp Glu Lys Lys
 230 235 240 245

gac atc atc gcc ttc atc aag tcc acc aag gag act cca tca cct ggt 883
 Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu Thr Pro Ser Pro Gly
 250 255 260

ggt tac tca ctc ggt agc ttg ggc cca gtg gct gag ggt ctg ttc atg 931
 Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala Glu Gly Leu Phe Met
 265 270 275

tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga 979
 Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly
 280 285 290

tca cgt tca tgagtaacaa caacgacaaa cag 1011
 Ser Arg Ser
 295

<210> 744
 <211> 296
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 744
 Met Met Glu Thr Asn Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys
 1 5 10 15

Pro Ser Ala Lys Lys Val Lys Asn Arg Arg Lys Val Arg Arg Thr Val
 20 25 30

Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
 35 40 45

Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
 50 55 60

Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
 65 70 75 80

Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
 85 90 95

Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
 100 105 110

Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
 115 120 125

Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
 130 135 140

Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu
 145 150 155 160

Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser

165	170	175
Ala Asp Val Ala Arg Gly Gly Asp	Leu Phe Arg Leu Asn Cys Ala Ser	
180	185	190
Cys His Asn Phe Thr Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr		
195	200	205
Ala Pro Asn Leu Asp Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met		
210	215	220
Leu Thr Gly Pro Gln Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser		
225	230	235
Ala Asp Glu Lys Lys Asp Ile Ile Ala Phe Ile Lys Ser Thr Lys Glu		
245	250	255
Thr Pro Ser Pro Gly Gly Tyr Ser Leu Gly Ser Leu Gly Pro Val Ala		
260	265	270
Glu Gly Leu Phe Met Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala		
275	280	285
Ala Met Trp Ile Gly Ser Arg Ser		
290	295	

<210> 745

<211> 502

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXN03096

<400> 745

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cgcaggcgcc gttgtcacct cactgctcac cttgtacacc atg gtt ctg gtc tgg	115
Met Val Leu Val Trp	
1 5	

tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc	163
Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr	
10 15 20	

gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc	211
Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala	
25 30 35	

gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc	259
Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe	
40 45 50	

tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca	307
Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala	
55 60 65	

gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat	355
-----------------------------------------------------------------	-----

Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp
 70 75 80 85
 gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat 403
 Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His
 90 95 100
 cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca 451
 His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser
 105 110 115
 acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg 499
 Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp
 120 125 130
 att 502
 Ile

<210> 746
 <211> 134
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 746
 Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala
 1 5 10 15
 Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile
 20 25 30
 Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro
 35 40 45
 Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
 50 55 60
 Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
 65 70 75 80
 Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
 85 90 95
 Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
 100 105 110
 Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
 115 120 125
 Asn His Asp Gln Trp Ile
 130

<210> 747
 <211> 504
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS

<222> (101)..(481)

<223> RXN02036

<400> 747

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gccctcatct ctgctgcagt ggcggctctc ggaggggtggt gtg cat att cct ttt 115
 Val His Ile Pro Phe
 1 5

ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
 Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
 10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
 105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 120 125

ttt 504

<210> 748

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

Val His Ile Pro Phe Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys
 1 5 10 15

Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala

50	55	60	
Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala			
65	70	75	80
Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile			
	85	90	95
Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg			
	100	105	110
Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn			
	115	120	125
<210> 749			
<211> 882			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(859)			
<223> RXN02765			
<400> 749			
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ttcaaccccat ggccgtatcc tcgcggattt taggagataa atg tct aat caa tta	115		
	Met Ser Asn Gln Leu		
	1	5	
ccc gat cac gtc cgc gac gcc ttc caa gta ggt gcg gga cct gcc gaa	163		
Pro Asp His Val Arg Asp Ala Phe Gln Val Gly Ala Gly Pro Ala Glu			
	10	15	20
caa ctc ggt caa gct tgg gac ttc gga ttc cgc gtc ggc aac act gtg	211		
Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg Val Gly Asn Thr Val			
	25	30	35
ttc gcc aaa gtg acg gcg ccg gaa gtg tcg ggc tgg tcg tcg aaa acc	259		
Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly Trp Ser Ser Lys Thr			
	40	45	50
cgc gaa acc ctg aaa cca gaa ggc gtg cgc gtc gta cga ccg atc cgc	307		
Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val Val Arg Pro Ile Arg			
	55	60	65
tcc acc gac ggc cga ttt gtg gtt gcg ggg tgg cgc gca tcg gtg ttc	355		
Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp Arg Ala Ser Val Phe			
	70	75	80
tct acg gga acg atc agc aag cga gtc gat gag acg gtc gtt gcg ggt	403		
Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu Thr Val Val Ala Gly			
	90	95	100
ctt cgt ttg gca gat gca tta gtg gat acg cat gca ccg gaa cct gtg	451		
Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His Ala Pro Glu Pro Val			
	105	110	115
gac aat gtg ttt aac cgt gct gat gtg cag gcc tgg gaa gag cag ccc	499		

Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala Trp Glu Glu Gln Pro
 120 125 130
 ggt cga atc ggt gaa ttg ttg gag ccg att aat cgc gtg aac cag gtt 547
 Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn Arg Val Asn Gln Val
 135 140 145
 ggt cat gcg gat atg ttg gcg aca acg ctg tat gcg gga act cag cca 595
 Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr Ala Gly Thr Gln Pro
 150 155 160 165
 cct gca gtg acg gat ttg gtg cca gtg ctg cgt ccg cat ggt ttc act 643
 Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg Pro His Gly Phe Thr
 170 175 180
 gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag 691
 Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu
 185 190 195
 gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt 739
 Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val
 200 205 210
 ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac 787
 Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn
 215 220 225
 aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc 835
 Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu
 230 235 240 245
 gtg tcg tat gtt tct gac aag att tgaggatatgt cggaatacaa acc 882
 Val Ser Tyr Val Ser Asp Lys Ile
 250

<210> 750

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly
 1 5 10 15
 Ala Gly Pro Ala Glu Gln Leu Gly Gln Ala Trp Asp Phe Gly Phe Arg
 20 25 30
 Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly
 35 40 45
 Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val
 50 55 60
 Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp
 65 70 75 80
 Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu
 85 90 95
 Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His

100	105	110
Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala 115 120 125		
Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn 130 135 140		
Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr 145 150 155 160		
Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg 165 170 175		
Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu 180 185 190		
Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu 195 200 205		
Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln 210 215 220		
Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg 225 230 235 240		
Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile 245 250		

<210> 751
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXN02206

<400> 751
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accttatgac ctcagtagtg tgggtggcgt gaaacagcga atg gtc ggt tca agt 115	
Met Val Gly Ser Ser	
1 5	
ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163	
Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser	
10 15 20	
ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211	
Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn	
25 30 35	
tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259	
Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val	
40 45 50	
gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307	
Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser	

55	60	65	
gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc			355
Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu			
70	75	80	85
ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat			403
Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp			
	90	95	100
gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg			451
Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val			
	105	110	115
ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg			499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu			
	120	125	130
gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga			547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly			
	135	140	145
tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca			595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala			
150	155	160	165
gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg			643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu			
	170	175	180
ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta			691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu			
	185	190	195
ggg gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act			739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr			
	200	205	210
gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca			787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr			
	215	220	225
gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc			835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile			
230	235	240	245
att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc			883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro			
	250	255	260
gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct			931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala			
	265	270	275
gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag			979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys			
	280	285	290
gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat			1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp			
295	300	305	

gtc tcc ctg tgacttggtc caattacatt cac
 Val Ser Leu
 310

1059

<210> 752
 <211> 312
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 752

Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr
 1 5 10 15
 Ser Thr Trp Gly Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe
 20 25 30
 Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn
 35 40 45
 Tyr Thr Thr Gly Val Ala Glu Met Leu Gly Thr Met Leu Asp Ala
 50 55 60
 Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn
 65 70 75 80
 Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu
 85 90 95
 Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu
 100 105 110
 Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu
 115 120 125
 Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr
 130 135 140
 Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala
 145 150 155 160
 Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln
 165 170 175
 Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro
 180 185 190
 Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly
 195 200 205
 Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser
 210 215 220
 Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp
 225 230 235 240
 Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly
 245 250 255
 Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg

260 265 270

Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu
275 280 285

Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr
290 295 300

Gln Ala Leu Asp Asp Val Ser Leu
305 310

<210> 753
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN02554

<400> 753

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ggataggctc cataaaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
Met Ser His Thr Lys
1 5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
10 15 20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
25 30 35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
40 45 50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
55 60 65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
70 75 80 85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
90 95 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
105 110 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
120 125 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
 Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
 135 140 145

 gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
 Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
 150 155 160 165

 att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
 Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
 170 175 180

 ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
 Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
 185 190 195

 aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 200 205

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 <213> Corynebacterium glutamicum

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 Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45

 Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60

 Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80

 Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95

 Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110

 Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125

 Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140

 Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160

 Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
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<222> (101)..(910)

<223> RXN01204

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 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

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 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu
 90 95 100

ccg atc ctg gcc acc atc ttc ttc gcg gct ctg ttg atg aac ctt gca 451
 Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu Leu Met Asn Leu Ala
 105 110 115

acg atc atc ccg gga cta aac atc tcc tcc aac tca cgt att gca ttc 499
 Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn Ser Arg Ile Ala Phe
 120 125 130

cca atc gtg atg gcg gta gct ggt tac atc gcg ttt atc tac gca ggc 547

Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala Phe Ile Tyr Ala Gly
 135 140 145

tct aag cgt tac gga ttc ttc aaa tat gtg aag tct tct gtt gtg att 595
 Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys Ser Ser Val Val Ile
 150 155 160 165

ccg aac att cca cca gca ctt cac gtc ttg gtg gtt cca att gag ttc 643
 Pro Asn Ile Pro Pro Ala Leu His Val Leu Val Val Pro Ile Glu Phe
 170 175 180

ttc tct aca ttc atc ttg agg cca gtc acc ctg gca ctg cgt ttg atg 691
 Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu Ala Leu Arg Leu Met
 185 190 195

gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca 739
 Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala
 200 205 210

acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc 787
 Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly
 215 220 225

gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt 835
 Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val
 230 235 240 245

atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att 883
 Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile
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 Glu Leu Ser Leu His Ala Asp Ser His
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taa 933

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 35 40 45
 Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50 55 60
 Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80
 Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95

Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
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 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
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 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205
 Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
 210 215 220
 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
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 Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
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 Met Lys Gly Glu Phe
 1 5
 cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20
 agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35
 ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259

Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val		
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gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307	
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro		
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cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggt	att	355	
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile		
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cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggt	cgt	cgg	ttc	ctg	403	
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu		
			90					95						100			
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451	
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala		
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Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe		
		120				125						130					
cca	atc	gtg	atg	gcg	gta	gct	ggt	tac	atc	gcg	ttt	atc	tac	gca	ggc	547	
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly		
	135					140					145						
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	gtt	gtg	att	595	
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile		
	150				155					160					165		
ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	gtt	cca	att	gag	ttc	643	
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe		
			170					175						180			
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691	
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met		
			185					190					195				
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	gtt	ctg	ctt	ttc	ttc	gca	739	
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala		
		200					205					210					
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787	
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly		
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gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	gtt	tac	gag	atc	att	gtt	835	
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val		
	230				235					240					245		
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862	
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<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 758

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Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
          35           40           45

Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
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Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
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Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
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Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
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Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
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Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
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Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
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Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
          165          170          175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
          180          185          190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
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Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
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Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
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Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala
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atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
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Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
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gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat 259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn
40 45 50

gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt 307
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu
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gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt 355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu
70 75 80 85

aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca 403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro
90 95 100

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Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro
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Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu
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ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg 547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu
135 140 145

gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt 595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly
150 155 160 165

cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc 643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val
170 175 180

tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac 691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp
185 190 195

aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc 739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly
200 205 210

tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc 787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu
215 220 225

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Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
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Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
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Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	
gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
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Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
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Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
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Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
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Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
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Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
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Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
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 Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln
 470 475 480 485

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 490 495 500

 aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc 1651
 Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr
 505 510 515

 cct gtc atc aac gag cct gag gtt gaa gca ctc gat gca ggc cag gtc 1699
 Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
 520 525 530

 aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741
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 35 40 45

 Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
 50 55 60

 Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
 65 70 75 80

 Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
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 Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
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 Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
 115 120 125

 Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
 130 135 140

 Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160

 Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
 165 170 175

Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
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 Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
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 Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
 210 215 220
 Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
 225 230 235 240
 Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
 245 250 255
 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
 275 280 285
 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
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 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
 305 310 315 320
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
 340 345 350
 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
 355 360 365
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 370 375 380
 Gly Met Lys Lys Val Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe
 385 390 395 400
 Arg Asp Leu Glu Ala Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala
 405 410 415
 Ser Lys Ser Gln Leu Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile
 420 425 430
 Gln Ser Glu Asn Ala Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu
 435 440 445
 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
 450 455 460
 Arg Arg Phe Glu Ser Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala
 465 470 475 480
 Gln Val Tyr Glu Gln Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser
 485 490 495

Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
 500 505 510

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Ser Lys Lys
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 <223> RXN01193

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 Met Thr Thr Ala Leu
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 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
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gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
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 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115

ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130

cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc	547
Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly	
135 140 145	
atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc	595
Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile	
150 155 160 165	
ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa	643
Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu	
170 175 180	
atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca	691
Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala	
185 190 195	
ggt gtt ggt gag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg	739
Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
200 205 210	
gaa gaa atg ggc gtt ctc cag gac acc gcc ctg gtg ttc ggt cag atg	787
Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
215 220 225	
gat gag cca cca gga gtc ggt atg cgc gtg gct ctg tcc ggc ctg acc	835
Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala Leu Ser Gly Leu Thr	
230 235 240 245	
atg gcg gag tac ttc cgc gat gtt cag aac cag gac gtg ctg ctg ttc	883
Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe	
250 255 260	
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Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr	
265 270 275	
ctt ctg ggt cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct	979
Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
280 285 290	
gac gag atg ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt	1027
Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
295 300 305	
tcg att acc tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc	1075
Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr	
310 315 320 325	
gac ccg gct cca gcg acc acc ttc gct cac ttg gat gca acc acc gag	1123
Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
330 335 340	
ctt gac cgc tcc att gct tcc aag ggt att tac cca gca gtg aac cca	1171
Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro	
345 350 355	
ctg acc tcc acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt	1219
Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
360 365 370	

cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag 1267
 His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys
 375 380 385

 gaa ctt cag gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa 1315
 Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu
 390 395 400 405

 gag gac aag atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg 1363
 Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu
 410 415 420

 ggt cag aac ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc 1411
 Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
 425 430 435

 tac gtg cca ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac 1459
 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
 440 445 450

 ggc gac ttc gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt 1507
 Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly
 455 460 465

 ttg gac gat gtc gaa gct gca tac aag aag ctg acc gga aag 1549
 Leu Asp Asp Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
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 taaggtagag acacatggct gaa 1572

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<211> 483

<212> PRT

<213> Corynebacterium glutamicum

<400> 762

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 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45

 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60

 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80

 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95

 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110

 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125

Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140
 Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu
 210 215 220
 Val Phe Gly Gln Met Asp Glu Pro Pro Gly Val Gly Met Arg Val Ala
 225 230 235 240
 Leu Ser Gly Leu Thr Met Ala Glu Tyr Phe Arg Asp Val Gln Asn Gln
 245 250 255
 Asp Val Leu Leu Phe Ile Asp Asn Ile Phe Arg Phe Thr Gln Ala Gly
 260 265 270
 Ser Glu Val Ser Thr Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr
 275 280 285
 Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr
 290 295 300
 Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala Val Tyr Val Pro
 305 310 315 320
 Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu
 325 330 335
 Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser Lys Gly Ile Tyr
 340 345 350
 Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala
 355 360 365
 Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile
 370 375 380
 Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met
 385 390 395 400
 Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg
 405 410 415
 Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr
 420 425 430
 Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe
 435 440 445
 Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro Glu Gln Ala Phe

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Thr Gly Lys			
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Tyr Phe Arg Asp Val Gln Asn Gln Asp Val Leu Leu Phe Ile Asp Asn			
15 20 25			
atc ttc cgt ttc acc cag gca ggt tct gag gtt tcc acc ctt ctg ggt			146
Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Thr Leu Leu Gly			
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cgt atg cct tcc gcc gtg ggt tac cag cca acc ctg gct gac gag atg			194
Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met			
45 50 55 60			
ggt gtt ctc cag gag cgc att acc tcc acc aag ggc cgt tcg att acc			242
Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr			
65 70 75			
tct ctg cag gcc gtt tac gtt cct gcc gat gac tac acc gac ccg gct			290
Ser Leu Gln Ala Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala			
80 85 90			
cca gcg acc acc ttc gct cac ttg gat gca acc acc gag ctt gac cgc			338
Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg			
95 100 105			
tcc att gct tcc aag ggt att tac cca gca gtg aac cca ctg acc tcc			386
Ser Ile Ala Ser Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser			
110 115 120			
acc tct cgt att ctc gag cca gca atc gtt ggt gag cgt cac tac gag			434
Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu			
125 130 135 140			
gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag gaa ctt cag			482
Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln			
145 150 155			
gac atc atc gcc atc ctt ggt atg gac gag ctt tct gaa gag gac aag			530

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
 160 165 170
 atc acc gtt gca cgt gcg cgt cgc atc gag cgc ttc ctg ggt cag aac 578
 Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn
 175 180 185
 ttc ttc gtt gca gag aag ttc acc ggt ctt cct ggc tcc tac gtg cca 626
 Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro
 190 195 200
 ctg acc gac acc gtc gac gct ttc gag cgt att tgc aac ggc gac ttc 674
 Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe
 205 210 215 220
 gac cac tac cca gag cag gct ttc aac ggc ctc ggt ggt ttg gac gat 722
 Asp His Tyr Pro Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp
 225 230 235
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 Val Glu Ala Ala Tyr Lys Lys Leu Thr Gly Lys
 240 245
 gaa 778

<210> 764
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 <213> Corynebacterium glutamicum

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 35 40 45
 Ala Val Gly Tyr Gln Pro Thr Leu Ala Asp Glu Met Gly Val Leu Gln
 50 55 60
 Glu Arg Ile Thr Ser Thr Lys Gly Arg Ser Ile Thr Ser Leu Gln Ala
 65 70 75 80
 Val Tyr Val Pro Ala Asp Asp Tyr Thr Asp Pro Ala Pro Ala Thr Thr
 85 90 95
 Phe Ala His Leu Asp Ala Thr Thr Glu Leu Asp Arg Ser Ile Ala Ser
 100 105 110
 Lys Gly Ile Tyr Pro Ala Val Asn Pro Leu Thr Ser Thr Ser Arg Ile
 115 120 125
 Leu Glu Pro Ala Ile Val Gly Glu Arg His Tyr Glu Val Ser Gln Arg
 130 135 140
 Val Ile Gly Ile Leu Gln Lys Asn Lys Glu Leu Gln Asp Ile Ile Ala
 145 150 155 160

Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys Ile Thr Val Ala
 165 170 175

Arg Ala Arg Arg Ile Glu Arg Phe Leu Gly Gln Asn Phe Phe Val Ala
 180 185 190

Glu Lys Phe Thr Gly Leu Pro Gly Ser Tyr Val Pro Leu Thr Asp Thr
 195 200 205

Val Asp Ala Phe Glu Arg Ile Cys Asn Gly Asp Phe Asp His Tyr Pro
 210 215 220

Glu Gln Ala Phe Asn Gly Leu Gly Gly Leu Asp Asp Val Glu Ala Ala
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Tyr Lys Lys Leu Thr Gly Lys
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 Met Thr Thr Ala Leu
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gaa gag cag aac gca cag cag gca gcc act gcc ggc cgt gtc gtg cgt 163
 Glu Glu Gln Asn Ala Gln Gln Ala Ala Thr Ala Gly Arg Val Val Arg
 10 15 20

gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
 25 30 35

gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
 40 45 50

aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
 55 60 65

cgc acc atc gct atg gca cca acc gac gga ctt gtc cgc ggt gct gct 355
 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
 70 75 80 85

gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
 90 95 100

aag ggc cac gta ttc aac gct ttg ggc gac tgc cta gac gac gtt tcc 451
 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
 105 110 115
 ctg aac aac aac cca gag atc gag cgt tgg ggc atc cac cgc gag cca 499
 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
 120 125 130
 cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
 135 140 145
 atc aag gtt atc gac ctt ctc acc cct tac gtt aag ggt gga aag atc 595
 Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
 150 155 160 165
 ggc ctc ttc ggt ggt gca ggt gtg ggt aag acc gtt ctt atc cag gaa 643
 Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr Val Leu Ile Gln Glu
 170 175 180
 atg atc acc cgt att gca cgt gag ttc tcc ggt act tcc gtg ttc gca 691
 Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly Thr Ser Val Phe Ala
 185 190 195
 ggt gtt ggt aag cgt acc cgt gag ggc acc gac ctc ttc ctc gaa atg 739
 Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met
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<210> 766

<211> 213

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 766

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 20 25 30
 Arg Gly Glu Leu Pro Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr
 35 40 45
 Leu Glu Ser Val Lys Lys Thr Val Val Leu Glu Val Ala Gln His Leu
 50 55 60
 Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
 65 70 75 80
 Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
 85 90 95
 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
 100 105 110
 Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
 115 120 125
 Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
 130 135 140

Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
 145 150 155 160
 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
 165 170 175
 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
 180 185 190
 Thr Ser Val Phe Ala Gly Val Gly Lys Arg Thr Arg Glu Gly Thr Asp
 195 200 205
 Leu Phe Leu Glu Met
 210

<210> 767
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(340)
 <223> RXN02821

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 Met Asn Glu Ile Ile
 1 5
 ctg gca cag gac gca acc gag tcc acc atc acc gga ctt ggc gct gtc 163
 Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
 10 15 20
 ggc tac ggc atc gca acc atc gga cct ggc ctc ggc atc ggc atc ctg 211
 Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
 25 30 35
 gtt ggt aag gct ctc gag ggt atg gca cgt cag cct gag atg gct gga 259
 Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
 40 45 50
 cag ctc cgt acc acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg 307
 Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
 55 60 65
 gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
 Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 70 75 80
 aag 363

<210> 768
 <211> 80
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 768

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Gly Ile Gly Ile Leu Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln
      35             40             45

Pro Glu Met Ala Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala
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Phe Val Glu Ala Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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<211> 303

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(280)

<223> FRXA02821

<400> 769

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                               Val Gly Tyr Gly Ile
                               1             5

gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
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ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
      25             30             35

acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
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<211> 60

<212> PRT

<213> Corynebacterium glutamicum

<400> 770

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 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(609)
 <223> RXA01200

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 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
 20 25 30
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480

Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
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 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
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 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
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 caa 632

<210> 772
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
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200

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Met Ala Glu Ile Thr																		
1 5																		
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Val Glu Leu Val Ser Val Glu Arg Met Leu Trp Ala Gly Gln Ala Ser																		
10 15 20																		
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Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile Gly Val Leu Pro Asp																		
25 30 35																		
cac gag cct ctt ctc ggc caa ttg gtt gag aac ggt gtc gtg acc atc																		259
His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn Gly Val Val Thr Ile																		
40 45 50																		
cag ccg atc gac ggc gaa aag ctt atc gcc ggc gtt tcg gat gga ttc																		307
Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly Val Ser Asp Gly Phe																		
55 60 65																		
ctc tcc gta tct aag gaa aag gtg acg atc ctc gcg gac ttc gcc gtc																		355
Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu Ala Asp Phe Ala Val																		
70 75 80 85																		
tgg gcg aat gag gtt gat acc gca tcc gcc gag gct gac ctt aat tcg																		403
Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu Ala Asp Leu Asn Ser																		
90 95 100																		
gac gac gag ctg gcc aag gca cac gcc gag gct ggg ctg cgc gcg gtc																		451
Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala Gly Leu Arg Ala Val																		
105 110 115																		
cgc cgc agc agc gaa ggt ctc taaacctccg tttagctgaa gta																		495
Arg Arg Ser Ser Glu Gly Leu																		
120																		

<400> 774
Met Ala Glu Ile Thr Val Glu Leu Val Ser Val Glu Arg Met Leu Trp
1 5 10 15

Ala Gly Gln Ala Ser Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile
 20 25 30

Gly Val Leu Pro Asp His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn
 35 40 45

Gly Val Val Thr Ile Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly
 50 55 60

Val Ser Asp Gly Phe Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu
 65 70 75 80

Ala Asp Phe Ala Val Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu
 85 90 95

Ala Asp Leu Asn Ser Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala
 100 105 110

Gly Leu Arg Ala Val Arg Arg Ser Ser Glu Gly Leu
 115 120

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<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01202

<400> 775

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taaatgactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt 115
 Met Ala Thr Ile Arg
 1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163
 Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr
 10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211
 Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly
 25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259
 Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu
 40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307
 Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu
 55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355
 Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg
 70 75 80 85

ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag 403

Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu Lys Lys Ala Ala Glu	
90 95 100	
ctg gaa aag ctt ctt gct gaa agt gga tac gaa gtg gtt cgt tat gtc	451
Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu Val Val Arg Tyr Val	
105 110 115	
acc ggc aaa aag ggc gtc gac tac tac aag ttc cgc gct gaa gat gtg	499
Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe Arg Ala Glu Asp Val	
120 125 130	
gct ggc acc tgg act gga ttc tca cag gat cca gac tgg gca gct acc	547
Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro Asp Trp Ala Ala Thr	
135 140 145	
cac aac gtg cgc cgt cac ctc att gat ggt ttc acc gcc agc tct gaa	595
His Asn Val Arg Arg His Leu Ile Asp Gly Phe Thr Ala Ser Ser Glu	
150 155 160 165	
ggt gaa gct gca tgg cgc gag gga ctg aac cta cca gaa ggc cag gat	643
Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu Pro Glu Gly Gln Asp	
170 175 180	
atc cag ggc ttc gac cag gtt cac gtg gtc tac acc gag ttc atc tcc	691
Ile Gln Gly Phe Asp Gln Val His Val Val Tyr Thr Glu Phe Ile Ser	
185 190 195	
atg ctg act caa aac cca gta gtg cac caa ctg ctg cct gtt gag cca	739
Met Leu Thr Gln Asn Pro Val Val His Gln Leu Leu Pro Val Glu Pro	
200 205 210	
gtc atc gaa gat gaa att ttc gaa aaa ggc gag gat ctg ctg tcc tct	787
Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu Asp Leu Leu Ser Ser	
215 220 225	
tcc ggc gaa gtc gaa ccc gac tac gag ttc gag ccg gat gca gac act	835
Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu Pro Asp Ala Asp Thr	
230 235 240 245	
ctg ctt gag gca ctg ctt ccg cag tac gtc tct cgt agg ctg ttc tcc	883
Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser Arg Arg Leu Phe Ser	
250 255 260	
atc ttc ttg gag gct gca gct gca gag tcc gct tca cgt cga aac gcg	931
Ile Phe Leu Glu Ala Ala Ala Glu Ser Ala Ser Arg Arg Asn Ala	
265 270 275	
atg aag tct gcg act gac aac gct acg gaa ctg gtc aag gac ctg tcc	979
Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu Val Lys Asp Leu Ser	
280 285 290	
cgt gtg gcc aac cag gca cgt cag gca cag atc acc cag gaa atc aca	1027
Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile Thr Gln Glu Ile Thr	
295 300 305	
gag att gtt ggt ggc gca ggc gcg ctc gcc gac agc gga gaa agt gac	1075
Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp Ser Gly Glu Ser Asp	
310 315 320 325	
taattatgac tacagctctt gaa	1098

<210> 776

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

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Thr Lys Lys Ile Thr Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile
 20 25 30

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu
 35 40 45

Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
 50 55 60

Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
 65 70 75 80

Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
 85 90 95

Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
 100 105 110

Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
 115 120 125

Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
 130 135 140

Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
 145 150 155 160

Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
 165 170 175

Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
 180 185 190

Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
 195 200 205

Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
 210 215 220

Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
 225 230 235 240

Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
 245 250 255

Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
 260 265 270

Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
 275 280 285

Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
 290 295 300

Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
 305 310 315 320

Ser Gly Glu Ser Asp
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<210> 777
 <211> 1773
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1750)
 <223> RXN02434

<400> 777
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 Met Arg Thr Phe Ala
 1 5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
 Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
 10 15 20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
 Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
 25 30 35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259
 Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
 40 45 50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
 Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
 55 60 65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
 Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
 70 75 80 85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
 Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
 90 95 100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
 Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
 105 110 115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta gcc gct 499
 Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
 120 125 130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
 Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile

135	140	145	
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gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu 170 175 180			643
ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu 185 190 195			691
gac gac aca gcc gta gat ttc ctc atc tcg gag att tcc cgt ttc aaa Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu Ile Ser Arg Phe Lys 200 205 210			739
ggt cca gtg ctg atc gcc agc cac gat cgc ttc ttc ctc gac tcc gtc Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe Phe Leu Asp Ser Val 215 220 225			787
tgt acc gag tta atc gac ctc gat cct gca ctt gga cct gag ggc gga Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu Gly Pro Glu Gly Gly 230 235 240 245			835
tcc ggc gaa gaa gta aaa caa gcc gtg tct ttt ggt ggt gga ttt tct Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe Gly Gly Gly Phe Ser 250 255 260			883
gaa tac atc aaa gaa cgc gag acc cgc cgc acc cgc tgg gct cag ttg Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr Arg Trp Ala Gln Leu 265 270 275			931
tac acc gca caa gaa acc gag cgg gaa aaa ctc gaa gaa acc acc ggc Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu Glu Glu Thr Thr Gly 280 285 290			979
acc acc gaa tcg gat att ttc cac agc tcg gtt tcc aaa tcg gaa gct Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val Ser Lys Ser Glu Ala 295 300 305			1027
aaa atc acc gcg aaa ttt tac gca gac cgg gca gct aaa act caa ggc Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala Ala Lys Thr Gln Gly 310 315 320 325			1075
aac cgc gtc cgc tcc gcc aaa aac cgc ctg aag gaa ttg gaa cgc tat Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys Glu Leu Glu Arg Tyr 330 335 340			1123
gaa atc cca gca cct cca aag cca ctg gaa ttc caa ggc atc cca gaa Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe Gln Gly Ile Pro Glu 345 350 355			1171
gcc tcc gga aac ggt cac ggt gaa aca cta gaa gtg cgg gct att gct Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu Val Arg Ala Ile Ala 360 365 370			1219
gtg gaa aac agg ctt caa ccc ttg act ttc cac atc gat ccc ggc gac Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His Ile Asp Pro Gly Asp 375 380 385			1267

cac atc ctg gtc gaa ggc ccc aac ggt gtc ggt aaa tcc acc ctg ctg 1315
 His Ile Leu Val Glu Gly Pro Asn Gly Val Gly Lys Ser Thr Leu Leu
 390 395 400 405

 agc gtt ctg gaa ggc gtg ctt gaa cca acc gaa ggt gaa ttg atc gtc 1363
 Ser Val Leu Glu Gly Val Leu Glu Pro Thr Glu Gly Glu Leu Ile Val
 410 415 420

 ccc gaa ggg ctg aaa gtt gcg cgc ctg aaa cag gac gat cag tgg acg 1411
 Pro Glu Gly Leu Lys Val Ala Arg Leu Lys Gln Asp Asp Gln Trp Thr
 425 430 435

 gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
 440 445 450

 aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
 455 460 465

 acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
 470 475 480 485

 cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
 490 495 500

 ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
 505 510 515

 gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
 520 525 530

 gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747
 Asp Arg Trp Ile Arg Lys Arg Trp Thr Gly Lys Lys Ile Ser Leu Ser
 535 540 545

 cgt taaaccctac tgaacaggaa cct 1773
 Arg
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<210> 778

<211> 550

<212> PRT

<213> Corynebacterium glutamicum

<400> 778

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 20 25 30

 Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
 35 40 45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
 50 55 60
 Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65 70 75 80
 Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
 85 90 95
 Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
 100 105 110
 Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp
 115 120 125
 Ala Ala Leu Gly Ala Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala
 130 135 140
 Arg Ile Glu Thr Ile Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg
 145 150 155 160
 Ser Thr Pro Ile Gly Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala
 165 170 175
 Leu Ala Ala Leu Leu Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu
 180 185 190
 Pro Thr Asn His Leu Asp Asp Thr Ala Val Asp Phe Leu Ile Ser Glu
 195 200 205
 Ile Ser Arg Phe Lys Gly Pro Val Leu Ile Ala Ser His Asp Arg Phe
 210 215 220
 Phe Leu Asp Ser Val Cys Thr Glu Leu Ile Asp Leu Asp Pro Ala Leu
 225 230 235 240
 Gly Pro Glu Gly Gly Ser Gly Glu Glu Val Lys Gln Ala Val Ser Phe
 245 250 255
 Gly Gly Gly Phe Ser Glu Tyr Ile Lys Glu Arg Glu Thr Arg Arg Thr
 260 265 270
 Arg Trp Ala Gln Leu Tyr Thr Ala Gln Glu Thr Glu Arg Glu Lys Leu
 275 280 285
 Glu Glu Thr Thr Gly Thr Thr Glu Ser Asp Ile Phe His Ser Ser Val
 290 295 300
 Ser Lys Ser Glu Ala Lys Ile Thr Ala Lys Phe Tyr Ala Asp Arg Ala
 305 310 315 320
 Ala Lys Thr Gln Gly Asn Arg Val Arg Ser Ala Lys Asn Arg Leu Lys
 325 330 335
 Glu Leu Glu Arg Tyr Glu Ile Pro Ala Pro Pro Lys Pro Leu Glu Phe
 340 345 350
 Gln Gly Ile Pro Glu Ala Ser Gly Asn Gly His Gly Glu Thr Leu Glu
 355 360 365
 Val Arg Ala Ile Ala Val Glu Asn Arg Leu Gln Pro Leu Thr Phe His

1100

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Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp	
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gag cgc atc ggc tac tgg gtg gta acc aaa tat gac gac atc aaa acc	307
Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr Asp Asp Ile Lys Thr	
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acc ttt gat gac tgg gaa aca ttc tcc tct gaa aat gca caa gcc cca	355
Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu Asn Ala Gln Ala Pro	
70 75 80 85	
gtc cgc aag cgt gga cct cag gca acc caa atc atg acc gat ggc ggc	403
Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile Met Thr Asp Gly Gly	
90 95 100	
ttc act gca tac tcc gga tta tca gct cgt att cca cca gag cac acc	451
Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile Pro Pro Glu His Thr	
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cgc atc cgc gca atc gca caa aag gcc ttc acg cca cgc cgc tat aaa	499
Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr Pro Arg Arg Tyr Lys	
120 125 130	
gca ctc gaa cca gat atc cga gca atg gtg att gat cgt gtg gag aaa	547
Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile Asp Arg Val Glu Lys	
135 140 145	
atg ttg gcg aat gat caa cac gtc ggc gat atg gtg tca gat ctt gcc	595
Met Leu Ala Asn Asp Gln His Val Gly Asp Met Val Ser Asp Leu Ala	
150 155 160 165	
tac gac att cca acc atc acg atc ctg acg ctg atc ggt gca gat att	643
Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu Ile Gly Ala Asp Ile	
170 175 180	
ttc atg gtg gtc acc tac aag cgg tgg tca gat tcc cgt gcg gcc atg	691
Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp Ser Arg Ala Ala Met	
185 190 195	
acc tgg ggc gat ctt agt gat gaa gag cag atc cca cac gca cac aat	739
Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile Pro His Ala His Asn	
200 205 210	
ttg gtt gag tac tgg cag gaa tgc caa cgc atg gta gct gat gca cat	787
Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met Val Ala Asp Ala His	
215 220 225	
gca cac ggt ggc gac aac ctc acc gct gat cta gtg cga gca cag caa	835
Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu Val Arg Ala Gln Gln	
230 235 240 245	
gag ggt caa gaa atc acc gat cat gag att gct tct ttg ctg tac tcc	883
Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala Ser Leu Leu Tyr Ser	
250 255 260	
ctg ctt ttt gcg ggg cac gaa aca acc acc acg ttg atc tcc aat tgt	931
Leu Leu Phe Ala Gly His Glu Thr Thr Thr Leu Ile Ser Asn Cys	
265 270 275	
ttc cga gtt ctc ctc gat cat cca gag cag tgg caa gcc att cta gag	979

Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp Gln Ala Ile Leu Glu
 280 285 290
 aat cca aaa ctg att cct gcg gca gtg gat gag gtc ttg cgg tac tcc 1027
 Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu Val Leu Arg Tyr Ser
 295 300 305
 ggc tcg atc gtg ggg tgg cgt cga aaa gca tta aaa gac acc gag atc 1075
 Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu Lys Asp Thr Glu Ile
 310 315 320 325
 ggc ggc gtt gcc att aag gaa ggc gat ggt gtt ctg ctg ctc atg ggt 1123
 Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val Leu Leu Leu Met Gly
 330 335 340
 tcc gcg aac cgc gat gaa gct cgc ttt gaa aat ggc gag gaa ttc gat 1171
 Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp
 345 350 355
 atc agc cgc gct aat gcg cgc gag cac ctg tct ttt ggt ttc ggc atc 1219
 Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile
 360 365 370
 cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt 1267
 His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys
 375 380 385
 ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac 1315
 Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp
 390 395 400 405
 aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct 1363
 Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser
 410 415 420
 gtt ccc gtg act tgg aac gct taacgcttta ttaaataagg aga 1407
 Val Pro Val Thr Trp Asn Ala
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<210> 780

<211> 428

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 780

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 Phe Gly His Thr Ser Glu Ser Thr Ser His His Gly Tyr Gln Pro Phe
 20 25 30
 Asp Met His Asn Pro Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu
 35 40 45
 Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr
 50 55 60
 Asp Asp Ile Lys Thr Thr Phe Asp Asp Trp Glu Thr Phe Ser Ser Glu
 65 70 75 80

Asn Ala Gln Ala Pro Val Arg Lys Arg Gly Pro Gln Ala Thr Gln Ile
 85 90 95
 Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile
 100 105 110
 Pro Pro Glu His Thr Arg Ile Arg Ala Ile Ala Gln Lys Ala Phe Thr
 115 120 125
 Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile
 130 135 140
 Asp Arg Val Glu Lys Met Leu Ala Asn Asp Gln His Val Gly Asp Met
 145 150 155 160
 Val Ser Asp Leu Ala Tyr Asp Ile Pro Thr Ile Thr Ile Leu Thr Leu
 165 170 175
 Ile Gly Ala Asp Ile Phe Met Val Val Thr Tyr Lys Arg Trp Ser Asp
 180 185 190
 Ser Arg Ala Ala Met Thr Trp Gly Asp Leu Ser Asp Glu Glu Gln Ile
 195 200 205
 Pro His Ala His Asn Leu Val Glu Tyr Trp Gln Glu Cys Gln Arg Met
 210 215 220
 Val Ala Asp Ala His Ala His Gly Gly Asp Asn Leu Thr Ala Asp Leu
 225 230 235 240
 Val Arg Ala Gln Gln Glu Gly Gln Glu Ile Thr Asp His Glu Ile Ala
 245 250 255
 Ser Leu Leu Tyr Ser Leu Leu Phe Ala Gly His Glu Thr Thr Thr Thr
 260 265 270
 Leu Ile Ser Asn Cys Phe Arg Val Leu Leu Asp His Pro Glu Gln Trp
 275 280 285
 Gln Ala Ile Leu Glu Asn Pro Lys Leu Ile Pro Ala Ala Val Asp Glu
 290 295 300
 Val Leu Arg Tyr Ser Gly Ser Ile Val Gly Trp Arg Arg Lys Ala Leu
 305 310 315 320
 Lys Asp Thr Glu Ile Gly Gly Val Ala Ile Lys Glu Gly Asp Gly Val
 325 330 335
 Leu Leu Leu Met Gly Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn
 340 345 350
 Gly Glu Glu Phe Asp Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser
 355 360 365
 Phe Gly Phe Gly Ile His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu
 370 375 380
 Gln Ala Lys Ile Cys Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu
 385 390 395 400
 His Leu Val Ala Asp Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe

405

410

415

Arg Val Pro Thr Ser Val Pro Val Thr Trp Asn Ala
420 425

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<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(955)
<223> RXN00387

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Met Phe Arg Ser Asn
1 5
att tcc tac gca gtc ggc gac gac atc caa aac gac cca gaa acc tgg 163
Ile Ser Tyr Ala Val Gly Asp Asp Ile Gln Asn Asp Pro Glu Thr Trp
10 15 20
gaa gac tac gaa ctt cgc gtc aac cac cca ctg cgc atc gaa ggc gac 211
Glu Asp Tyr Glu Leu Arg Val Asn His Pro Leu Arg Ile Glu Gly Asp
25 30 35
cgc gtc tac ctt cag ggc cac ggc ttc gcc cca aca ttc acc gtg acc 259
Arg Val Tyr Leu Gln Gly His Gly Phe Ala Pro Thr Phe Thr Val Thr
40 45 50
tgg cca aat ggc gag acc cgc acc cag acc gtg cag tgg cgc cca gac 307
Trp Pro Asn Gly Glu Thr Arg Thr Gln Thr Val Gln Trp Arg Pro Asp
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gac ccg acc ttc ttc ctg tcc tca ggc gtg gtc cgt ttc gat cca ccc 355
Asp Pro Thr Phe Phe Leu Ser Ser Gly Val Val Arg Phe Asp Pro Pro
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gcc ggc atg tac cca gac ctt tac gag cgc cgc caa aac cag ttg gcc 403
Ala Gly Met Tyr Pro Asp Leu Tyr Glu Arg Arg Gln Asn Gln Leu Ala
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atc cag gga ctt ttc gca ccg acc gcg gaa tgg gaa ggc gac aac aac 451
Ile Gln Gly Leu Phe Ala Pro Thr Ala Glu Trp Glu Gly Asp Asn Asn
105 110 115
gaa ctg ctg acc tcc tcc tac ccg gcg atg cgt gac cca gcc gtg gcg 499
Glu Leu Leu Thr Ser Ser Tyr Pro Ala Met Arg Asp Pro Ala Val Ala
120 125 130
atc gat att tac cgc ggc gac aat ggc ctc gat acc ggc atc gga cag 547
Ile Asp Ile Tyr Arg Gly Asp Asn Gly Leu Asp Thr Gly Ile Gly Gln
135 140 145
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Ser Leu Phe Ser Leu Asp Ser Ser Leu Met His Ser Gly Val Leu Gln

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Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser Glu Phe Ala Asn Tyr				
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Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val Leu Val Thr Thr Val				
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Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met Ile Arg Arg Arg Arg				
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Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly Thr Thr Arg Val Glu				
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Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys Glu Glu Asp Glu Asp				
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<210> 782

<211> 285

<212> PRT

<213> Corynebacterium glutamicum

<400> 782

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		20						25					30		

Arg	Ile	Glu	Gly	Asp	Arg	Val	Tyr	Leu	Gln	Gly	His	Gly	Phe	Ala	Pro
		35					40					45			

Thr	Phe	Thr	Val	Thr	Trp	Pro	Asn	Gly	Glu	Thr	Arg	Thr	Gln	Thr	Val
	50					55					60				

Gln	Trp	Arg	Pro	Asp	Asp	Pro	Thr	Phe	Phe	Leu	Ser	Ser	Gly	Val	Val
	65				70					75				80	

Arg	Phe	Asp	Pro	Pro	Ala	Gly	Met	Tyr	Pro	Asp	Leu	Tyr	Glu	Arg	Arg
				85					90					95	

Gln	Asn	Gln	Leu	Ala	Ile	Gln	Gly	Leu	Phe	Ala	Pro	Thr	Ala	Glu	Trp
			100					105						110	

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 Ser Gly Val Leu Gln Lys Ile Glu Arg Val Asn Leu Gln Ile Gly Asp
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 Thr Val Thr Leu Asp Asp Gly Thr Thr Val Ser Phe Asp Gly Ala Ser
 180 185 190
 Glu Phe Ala Asn Tyr Gln Ile Ser Arg Asp Pro Thr Gln Asn Trp Val
 195 200 205
 Leu Val Thr Thr Val Ile Ser Leu Val Ser Leu Val Gly Ser Leu Met
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 Ile Arg Arg Arg Arg Ile Trp Val Arg Phe Tyr Pro Gln Glu Asn Gly
 225 230 235 240
 Thr Thr Arg Val Glu Thr Gly Gly Leu Ala Arg Thr Asp Arg Ala Gly
 245 250 255
 Trp Gly Gly Glu Tyr Glu Lys Phe His Arg Glu Leu Leu Gly Leu Lys
 260 265 270
 Glu Glu Asp Glu Asp Glu Glu Tyr Phe Asp His Asp Asp
 275 280 285

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(54) Title: *CORYNEBACTERIUM GLUTAMICUM* GENES ENCODING PROTEINS INVOLVED IN CARBON METABOLISM AND ENERGY PRODUCTION

(57) Abstract: Isolated nucleic acid molecules, designated SMP nucleic acid molecules, which encode novel SMP proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing SMP nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated SMP proteins, mutated SMP proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of SMP genes in this organism.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00943

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/31 C12N15/55 C12N1/21 C12N9/18 C07K14/34
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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K C12P C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, EMBL

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PETERS-WENDISCH ET AL: "Pyruvate carboxylase as an anaplerotic enzyme in <i>Corynebacterium glutamicum</i> " MICROBIOLOGY, SOCIETY FOR GENERAL MICROBIOLOGY, READING, GB, vol. 143, no. PART 04, April 1997 (1997-04), pages 1095-1103, XP002110209 ISSN: 1350-0872 the whole document	1-3, 8-19, 22-34
X	EIKMANN ET AL: "The phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : molecular cloning, nucleotide sequence, and expression" MOL. GEN. GENET., vol. 218, 1989, pages 330-339, XP002138580 the whole document	1-3, 8-19, 22-34
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☒ Further documents are listed in the continuation of box C.☐ Patent family members are listed in annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"Z" document member of the same patent family

Date of the actual completion of the international search

2 November 2000

Date of mailing of the international search report

08.02.01

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Authorized officer

Galli, I

INTERNATIONAL SEARCH REPORT

International Application No

PCT/IB 00/00943

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	DATABASE EMBL SEQUENCES [Online] Accession No. 006814, 1 November 1997 (1997-11-01) COLE S.T.: "6-phosphogluconolactolase (6PGL) of Mycobacterium tuberculosis" XP002151659 52% identity at the amino acid level (Seq. 2) and 60% at nucleotide level (seq. 1). & COLE S.T. ET AL.: "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence" NATURE, vol. 393, 1998, pages 537-544, XP002151645 ---	6-17,37, 38
A	BATHE B. ET AL.: "A physical and genetic map of the Corynebacterium glutamicum ATCC13032 chromosome" MOL. GEN. GENET., vol. 252, 1996, pages 255-265, XP002151646 the whole document, in particular table 3. -----	1-38

INTERNATIONAL SEARCH REPORT

International application No.
PCT/IB 00/00943

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

see subject 1. on extra sheet

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-38, partly

An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an SMP protein or a portion thereof, said nucleic acid being characterized by seq. ID 1. An isolated nucleic acid comprising a nucleotide sequence at least 50% homologous to seq. 1. Corresponding polypeptides (seq. 2.). Corresponding vectors, recombinant host cells, production methods. Use in diagnosis of *C. diphtheriae*.

2-293. Claims 1-38, partly

Idem as subject-matter 1, but limited to the pairs of sequences listed in Table 1 (except those disclaimed).